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Q9ngw8 homo sapien Q9mjd7 canis famil Q9mjd2 m cyclic-nu Q80x18 mus musculu G35788 rattus norv G4536 homo sapien G4536 homo sapien G9157 rattus norv G7165 bos taurus G7765 bos taurus G7861 tetraodon n Q4445 tetraodon n G4445 tetraodon n G4445 tetraodon n G4671 tetraodon n G4671 cerochabdi G5237 caenorhabdi G6237 caenorhabdi G5237 caenorhabdi G5344 mcgmp-gate G3341 mcgm
                                                                                                                                           December 21, 2005, 19:46:59; Search time 234 Seconds (without alignments) 2439.198 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                1 MFKSLTKVNKVKPIGENNEN......PSAEGGEEVLTIEVKEKAKQ 809
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                      2166443 seqs, 705528306 residues
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043636 HUMAN

CMGB1 HUMAN

055157 RAT

077669 BOVIN

077659 BOVIN

077669 EDVIN

077669 TETNG

048KK5 TETNG

048KK1 TETNG

048KK5 TETNG

048KK5
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CNGB3_CANFA
CNGB3_MOUSE
QBOXL8_MOUSE
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Maximum Match 100%
Listing first 45 summaries
                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Match Length
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oryctolagus	sus scrota	h cgmp-gate	homo sapien	ictalurus p	rattus norv	rattue norv	rattus norv	rattus norv	rattus norv	c cdmp-dare	b cgmp-gate	bos taurus	mus musculu
028718	O9n0h4	P29973	04w5e3	P55934	09qwn7	09er32	09er33	000195	054997	028279	000194	029441	080×h6
CNGA2_RABIT	Q9NOH4 PIG	CNGA1 HUMAN	Q4W5E3 HUMAN	CNG ICTPU	Q9QWN7 RAT	Q9ER32_RAT	Q9ER33 RAT	CNGA2 RAT	Q549G7 RAT	CNGA1 CANFA	CNGA1_BOVIN	CNGA3_BOVIN	Q80XH6_MOUSE
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664	989	989	690	682	611	632	670	664	664	691	9	706	664
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818.5	818	817	817	807.5	908	806	806	804	804	801.5	797	794	789.5
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ALIGNMENTS

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MFKSLTKVNKVKPIGENNENEQSSRRNEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTPV
                                                                                                                   APVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPVKESDDKP
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   MPKSLTKVNKVKPIGENNENEQSSRRNEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTPV
                                                           TSEEPHTNIQDKLSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPA
                                                                                      TSEEPHTNIODKLSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPA
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                                                                                                                                                                             TEHYYRLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLAYNWNCWF1P1,R1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cyclic-mucleotide-gated cation channel beta 3 (CNG channel beta 3)
(Cyclic nucleotide gated channel beta 3) (Cone photoreceptor cGMP-gated channel beta subunit) (Cyclic nucleotide cation channel beta subunit)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO0889; CNMP BINDING 1; 1.
PROSITE; PSO0899; CNMP BINDING 2; 1.
PROSITE; PSO042; CNMP BINDING 3; 1.
Alternative splicing; 7GMP; 7GMP-binding; Disease mutation; GMP; Alternative in transport; Ionic channel; Multigene family; Nucleotide-binding; Polymorphism; Sensory transduction; Transmembrane;
                                                                                                              -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
-1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                     colorblindness mainly because of the consistent concurrence of
Isold=Q9NQW8-2; Sequence=VSP_009742;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed specifically in the retina.
DISEASE: Defects in CNGB3 are a cause of achromatopsia 3 (ACHM [MIM:262300]; also known as Pingelapsee blindness. ACHM3 is a congenital complete achromatopsia and is distinct from total
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/FTd=VAR 018110.
S -> P (in ACHM3).
/FTIG=VAR 018111.
E -> G (in dbSNP:3735972).
/FTIG=VAR 018112.
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AC23B7072C1C7DB3 CRC64;
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H3 (Potential).
Extracellular (Potential)
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P (in dbSNP:4961206)
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H5 (Potential).
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(By similarity).
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EMBL; AF228520; AAF80179.1; ALT_INIT; MRNA.
Ensembl; ENSG0000170289; Homo Sapiens.
HGNC; HGNC.2153; CNGB3.
MIM; 605080; -.
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Best Local Similarity
Matches 809; Conserv
                                                                                                  severe myopia.
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                                                                                           54 VTFEESHAKAQDKISEKNSLRDLTTNPNHQHPTESKGAMSEQKEMETGKEGLVSPKSKPL 113
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53
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                                                                                                                                                                                                                                                                                                                           VRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLL
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                                                                                                                                                   120 AAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPVKESDDK
                                                                                                                                                                                                                             180 -PTEHYYRLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLAYNWNCWFIPL
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
MFKSLT-KVNKVKPIGENNENEQSSRRNEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Cyclic-nucleotide-gated cation channel beta 3 (CNG channel beta 3)
Gyclic nucleotide gated channel beta 3) (Cone photoreceptor cGMP-gated channel beta 3) (Cone photoreceptor cGMP-modulatory subunit) (Cyclic nucleotide-gated cation channel
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Mus musculus (Mouse).
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                                                                                                                                                 Thum. Mol. Genet. 11:1823-1833 (2002).

-!- FUNCTION: Visual signal transduction is mediated by a G-protein coupled cascade using CGMP as second messenger. This protein can coupled cascade using CGMP which leads to an opening of the cation channel and thereby causing a depolarization of rod photoreceptors. Induced a flickering channel gating, weakened the putch rectification in the presence of extracellular calcium, increased sensitivity for L-cis diltiazem and enhanced the CAMP efficacy of the channel when coexpressed with CNGA3. Essential for the generation of light-evoked electrical responses in the red-, green- and blue sensitive complex with CNGA3 (By similarity).

-!- SUBUNIT. Heteroollgomeric complex with CNGA3 (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- DISEASE: Defects in CNGB3 are a cause of come degeneration (cd).
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                                                                                                                     ů
                                                                                                                                                                                                                                                                                                                                                                                                                                             function. This autosomal recessive disorder occurs naturally in the Alaskan Malamute and German Shorthaired Pointer breeds. SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family. SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
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PROSITE; PS00889; CNMP_BINDING_1; 1.
PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1.
CGMP; CGMP-binding; Disease mutation; Ion transport; Ionic channel; Multigene family; Nucleotide-binding; Sensory transduction; multigene family; Nucleotide-binding; Sensory transduction; ryanemembrane; Transport; Vision.
Cvtoplasmic (Potential).
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             NUCLECTIDE SEQUENCE [MRNA], AND VARIANT CD ASN-262. Pubmed=12140185; DOI=10.1093/hmg/ll.16.1823; Sidjanin D.J., Lowe J.K., MCElwee J.L., Milne B.S., Phippen T.M., Sargan D.R., Aguirre G.D., Acland G.M., Ostrander E.A.; "Canine CMSE3 mutations establish cone degeneration as orthologous the human achromatopsia locus ACHM3."; Mol. Genet. 11:1821-1822
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H6 (Potential).
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Extracellular (Potential)
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CGMP (By similarity).

CGMP (By similarity).

CGMP (By similarity).
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57; Mismatches 105;
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Ensembl; BNGSAG0000008906; Canis familiaris.
InterPro; IPR00595; CNMP bd.
InterPro; IPR005821; Ion Trans.
InterPro; IPR001622; K-channel pore.
Pfam; PF00027; CNMP binding; 1.
Pfam; PF00520; Ion Trans; 1.
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01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
 68.78;
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Q80XL8;
                 485; Conservative
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                                    NUCLECTIDE SEQUENCE.

YETAIN=CSTBL/6; TISSUE-Retina;

X MEDLINE=20130346; PUNNCHION, SUBUNIT, AND TISSUE SPECIFICITY.

X Geretner A., Zong X., Hofmann F., Biel M.;

Molecular cloning and functional characterization of a new modulatory cyclic nucleotide-gated channel subunit from mouse retina.";

TWO be activated by CAPP which leads to an opening of the cation coupled caecade using cGMP as second messenger. This protein can be activated by CGMP which leads to an opening of the cation channel and thereby causing a depolarization of rod photoreceptors. Essential for the generation of 19th-evoked photoreceptors. Essential for the generation of 19th-evoked colectrical responses in the red-, green- and blue sensitive cones (By similarity). Induced a flickering channel gating, weakened the outward rectification in the presence of extracellular calcium, increased sensitivity for L-cis diltiazem and enhanced the CAMP (CC) efficacy of the channel when coexpressed with CNGA3.

--- SUBUNIT: Heterooligomeric complex with CNGA3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ243572; CAB71152.1; -; mRNA.
Ensembl; ENSWUSG0000056494; Mus musculus.
MGI, MGI.1353562; CngB3.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0016021; C:integral to membrane; IC.
GO; GO:0010523; F:intracellular cGMP activated cation channel. . .; IPI.
GO; GO:0003187; P:3',5'-cGMP binding; IC.
GO; GO:0003187; P:intracellular cGMP activated cation channel. . .; IPI.
InterPro; IPR000581; ION Exans.
InterPro; IRR001622; K-channel_pore.
Pfam; PF00027; CNMP_binding; I.
Fran; PF00027; CNMP_binding; I.
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-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
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PROSITE; PS00888; CNMP BINDING 1; 1.

PROSITE; PS00889; CNMP_BINDING 2; 1.

PROSITE; PS50042; CNMP_BINDING 3; 1.

CGMP; CGMP-Dinding; Glycoprotein; Ion transport; Ionic channel; Multigene family; Nucleotide-binding; Sensory transduction; Iransmembrane; Transport, Vision.
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                                 FUNCTION, SUBUNIT, AND TISSUE SPECIFICITY
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Extracellular (Potential)
H4 (Potential).
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H5 (Potential).
Extracellular (Potential)
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                                                       1 MFKSLT-KVNKVKPIGENNENEQSSRRNEEGSHP--SNQSQQTTAQEENKGEEKSLKTKS
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                        1 MLKSLTVKFNKVNPM------EGRMEKKLCPNLSSLSOPTIAOGDNQSEKEPLRSR-
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GEQTLSVEVLEEKKE 863
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Socies M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garanatne P.H.,
Richards S., Worley K.C., Hale S., Garanatne P.H.,
A Richards S., Worley K., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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46.6%; Score 1971.5; DB 2; Length
Best Local Similarity 47.5%; Pred. No. 1.7e-106;
Matches 406; Conservative 107; Mismatches 247; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Sauter A., Biel M., Hofmann F.;
"Molecular cloning of cyclic nucleotide-gated cation channel subunits from pineal gland.";
Mol. Brain Res. 47:171-175(1997).
EMBL; AJ000496; CAA04133.1; -; mRNA.
HSSP; O88703; 1043.
Ensembl; ENSRNOG00000013544; Rattus norvegicus.
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NFS11SKVDLFKGCDTOM1YDMLLRLKSVLYLPGDFVCKKGE1GKEMY11KHGEVOVLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDGTKVLVTLKAGSVFGEISLLAAGGGNRRTANVVAHGFANLLTLDKKTLOEILVHYPDS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
                                                                                                                                                              FRACMDDTIAYMINYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFAD64A6A81AB49A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDISCULL, CASTON CONTROLL STATES OF CASTON C
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Length 1339;

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DB

cGMP-gated

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The beta subunit of human rod photoreceptor cGMP-gated cation channel
is generated from a complex transcription unit.";

EBBS Lett. 389:213-218(1996).

REBS, ARC04248; AAC04830.1; -; mRNA.

PIR; S12538; S12538.

PIR; S69275; S69275.

RISSP, O88703; 1043.

Brosembl; ENSG0000070729; Homo sapiens.

GO; GO:0005276; Fligand-gated ion channel activity; TAS.

GO; GO:000520; Prisansport; TAS.

GO; GO:000501; P:visual perception; TAS.

InterPro; IPR00522; K+channel_pore.

InterPro; IPR001622; K+channel_pore.

Ffam; PP00027; CMP binding; 1.

Rem; PP00027; CMP binding; 1.
     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                 NUCLECTIDE SEQUENCE.
Grunwald M.E., Yu W.P., Yu H.H., Yau K.W.;
"Identification of a domain on the beta subunit of the rod cGMP-cation channel that mediates inhibition by calcium-calmodulin.";
J. Biol. Chem. 0:0-0(1998).
                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDLINES6338110; PubMed=8766832; DOI=10.1016/0014-5793(96)00588-Ardell M.D., Aragon I., Oliveira L., Porche G.E., Burke E.,
Pittler S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1245;
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al Similarity 46.1%; Score 1952; DB 2; Length 1;
al Similarity 46.4%; Pred. No. 3.7e-105;
405; Conservative 121; Mismatches 237; Indels
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| S21 ALSPAESPVVAWSDPTTPKDTDGQDRAASTASTNSAIIND
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PROSITE; PS00889; CNMP_BINDING 2; 1.
PROSITE; PS50042; CNMP_BINDING 3; 1.
                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                             SPVVAWSDPTTPQEADGEDRAASTASQNSAIIND----RLQELVKMFKERTEKVKEKLID 684
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                                                                        VKPIGENNENEQSSRRNEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTPVTSEEPHTNIQ
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                            Indels 102;
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043636 HUMAN PRELIMINARY; PRT; 1245 AA.
AC 043636.
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rod photoreceptor CNG-channel beta subunit.
GN Name=RCNC2;
     ed. No. 1.6e-105;
Mismatches 240;
                                                                                                                                                                                 DKLSKKNSSGDLTTNPDPQN----AAEPTGTVP-
     Pred. No.
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                            Conservative 121;
     46.38;
Best Local Similarity
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----OPPOSIDPLTNLMYVLWLFFFVVMAMNWNCWLIPVRWAFPYQTPDNIHHWULMDYLC 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 VEDTDADSCPLMAEENPPS--TVLPPPSPAKSDTLIVPSSASGTHRKKLPSEDDEAEELK 184
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                                                          GO; GO: 0017071; C:intracellular cyclic nucleotide activated C. . .;
GO; GO: 0005222; F:intracellular cAMP activated cation channel. . .;
InterPro: IPR000592; cMMP_Ddd.
InterPro: IPR000592; cMMP_Ddd.
InterPro: IPR001622; K+channel_pore.
Pfam; PF0007; cMMP_Dinding; 1.
Pfam; PF00520; Ion_trans. I.
PROSITE; PS00889; CMMP_BINDING_1; 1.
PROSITE; PS00889; CMMP_BINDING_2; 1.
PROSITE; PS0042; CMMP_BINDING_3; 1.
PROSITE; PS0042; CMMP_BINDING_3; 1.
Alternative splicing; CAMP' cAMP-binding; lon transport;
Ionic channel; Multigene family; Nucleotide-binding; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 IQDK-----LSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    688 CAMP (Potential).
700 CAMP (Potential).
286 Missing (in isoform RCNC2A).
7 FTId=VSP 001110.
102285 MW; DC0E75433686EDDD CRC64;
                                                                                                                                                                                                                                                                      Cytoplasmic (Potential).
H1 (Potential).
Extracellular (Potential).
H2 (Potential).
Cytoplasmic (Potential).
H3 (Potential).
H4 (Potential).
Cytoplasmic (Potential).
H4 (Potential).
Cytoplasmic (Potential).
H5 (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
cAMP (By similarity).
Poly-Glu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 46.2%; Pred. No. 3.58-1UD;
Matches 403; Conservative 122; Mismatches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.0%; Score 1949; DB 1; 46.2%; Pred. No. 3.6e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         H6 (Potential).
EMBL; L15297; AAA65619.1; -; Genomic_DN
Ensembl; ENSG0000070729; Homo sapiens.
HGNC; HGNC:2151; CNGB1.
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                                                                                                                                                                                              1052
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                                                                                                                                                              620
                                                                                                                                                                                                                                                                                              681 GGTGKAS------LARLLKLKREQAAQKKENSEGEEEGKENEDKQKENEDKQK 728
                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is
                                                                                                                 MEDLINE=93226050; PubMed=7682292; DOI=10.1038/36276480;
Chen T.Y., Peng Y.-W., Dhallan R.S., Ahamed B., Reed R.R., Yau K.-W.;
"A new subunit of the cyclic nucleotide-gated cation channel in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family. SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
   GSTHWVYDGVGNSYIRCYYFAVKTLITIGGLPDPKTLFEIVFQLLNYFTGVFAFSVMIGQ
                                                                                                                                                                MY I KHGEVQVLGGPDGTKVLVTLKAGSVFGE I SLLAAGGGNRRTANVVAHGFANLLTLD
                                                                                                                                                                                                                                                                                                              MRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLK
                                                                                                 501 TLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKE
                                                                                                                                                                                                                              KKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLFPPKEETPKLFKTLL
                                                                                                                                                                                                                                                                                                                                                           729 BNEDKGKE-NEDKDKGREPEEKP-----LDRPECTASPIAVEEEPHSVRTVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   014028; 014029; 01-0029; 01-0029; 01-002-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAY-2005 (Rel. 47, Last annotation update) 05-005 (Rel. 47, CNG-4) (CNG-4) (CNG-4) (CYClic nucleotide-gated cation channel modulatory subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCNILT: Heterooligomeric complex with CNG1.
-:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- ALTERNATUP PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE (ISOFORMS RCNC2A AND RCNC2B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=CNGB1; Synonyms=CNCG4;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A new subunit or cue cyrretinal rods.";
Nature 362:764-767(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=RCNC2A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pittler S.J.;
"The beta subunit of human rod photoreceptor cGMP-gated cation channel
if a generated from a complex transcription unit.";

the beta subunit of human rod photoreceptor cGMP-gated cation channel
if a generated from a complex transcription unit.";

the personal sect. 389:213-218(1996).

R EMBL, US8837, AAB63387.1; -; mRNA.

R FASP, O88703; 1043.

R HSRP, O88703; 1043.

R HSRP, O88703; 1043.

R HSRP, CMGBL.

R GO; GO:0016621; C.integral to membrane; IEA.

DR GO; GO:00166225; F:3'.5'-cGMP binding; IEA.

DR GO; GO:0005216; F:ion channel activity; IEA.

DR GO; GO:0000166; F:nucleotide binding; IEA.
                                                                           929
                                                                                                                                            680
        MRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLK 500
                   560
                                                                                               MYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGGGNRRTANVVAHGFANLLTLD 620
                                                                                                                      716
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                  TLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKE
                                                              KKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLFPPKEETPKLFKTLL
                                                                                                                                                                                                        772 AMTGKWGGKGAKGGKLAHLRARLKELAALEAAAKHEEL---VEQAKSSQDVKGEEGSAAP
                                                                                                                                                                                                                                                 "cDNA, gene structure, and chromosomal localization of human GARI (CNCG3L), a homolog of the third subunit of bovine photoreceptor cGMP-
                                                                                                                                                               KKDLNEILVHYPESOKLLRKKARRMLRSNNK----PKEEKSVLILPPRAGTPKLFNAAL
                                                                                                                                                                                                                                  ENEDKGKE-NEDKOKGREPEEKPLDRPECTASPIAV------EEEPHSVRRTVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96338110; PubMed=8766832; DOI=10.1016/0014-5793(96)00588-1;
Ardell M.D., Aragon I., Oliveira L., Porche G.E., Burke E.,
                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96070429; PubMed=7590744;
Ardell M.D., Makhija A.K., Oliveira L., Miniou P.,
Viegas-Pequignot E., Pittler S.J.;
                                                                                                                                                                                                                                                                             777 RGTSRQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809
                                                                                                                                                                                                                                                                                            PRT; 1251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 CGMP-gated cation channel beta subunit
Name=CNGB1; Synonyms=CNCG2;
                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                          Q9UMG2 HUMAN PRELIMINARY;
Q9UMG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gated channel.";
Genomics 28:32-38(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

46.0%; Score 1949; DB 2; Length 1251;
Best Local Similarity 46.2%; Pred. No. 5.5e-105;
Matches 403; Conservative 122; Mismatches 238; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                 4701C53DB13C9055 CRC64;
GO, GO:0005267; F:potassium channel activity; IEA. GO; GO:0006811; P:lon transport; IEA. GO; GO:0006811; P:lon transport; IEA. GO; GO:0006811; P:lotassium ion transport; IEA. GO; GO:0007601; P:visual perception; IEA. InterPro; IPR005821; Ion_transport IEA. InterPro; IPR005821; Ion_transport InterPro; IPR005821; Ion_transport InterPro; IPR001622; K+channel_pore. Pfam; PF00027; CNWP binding; 1. Fam; PF00027; CNWP binding; 1. SMART; SM00100; cNMP; 1. PROSITE; PS000888; CNMP_BINDING_1; IUKNOWN_1. PROSITE; PS000889; CNMP_BINDING_3; 1. SEQUENCE 1251 AA; 139604 MW; 4701C53DB13C9055
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                PPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLS----SPEASPQTAKPTAVPPV 173
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                                                        K--ESDDKPTEHYYRLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLAYNW
                                                                                                              NCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLOFVRGGDIIVDSNELR
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE=98345361; PubMed=9679145; DOI=10.1083/jcb.142.2.473;
Wiesner B., Weiner J., Middendorff R., Hagen V., Kaupp U.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Cyclic nucleotide-gated channel beta subunit lc.
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HSSP; O88703; 1043.
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J. Cell Biol. 142:473-484(1998)
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                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley, TISSUE=Olfactory epithelium,
MEDLINE=98208604; PubMed=9539801; DOI=10.1073/pnas.95.8.4696;
Sautter A., Zong X., Hofmann F., Biel M.;
"An isoform of the rod photoreceptor cyclic nucleotide-gated channel beta subunit expressed in olfactory neurons.";
Proc. Natl. Acad. Sci. U.S.A. 95:4696-4701(1998).
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    DQHTHPKEAATDPPAPRTPPEPP-GSPPSSPPASLGSCEGEEGPAEPEEHSVR-
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MEDLINE=99307326; PubMed=10377344;
Bonigk W., Bradley J., Muller F., Sesti F., Boekhoff I., Ronn Kaupp U.B., Frings S.;
"The native rat olfactory cyclic nucleotide-gated channel is of three distinct subunits.";
J. Neurosci. 19:5332-5347(1999).
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                                                                                                                                                                                                      (Cyclic
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, A7000515; CAA04152.1; -; mRNA.
EMBL, AF066517; AAC19120.1; -; mRNA.
HSSP, O88703; 1Q43.
ENSENOGO000013544; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Cyclic nucleotide-gated cation channel beta subunit nucleotide-gated channel beta subunit lb).
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llarity 47.3%; Pred. No. 1.1e-103;
Conservative 114; Mismatches 228;
                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0006811; F:ion transport; IEA.
InterPro; IPR000582; cMMP_binding.
InterPro; IPR005821; Ion trans.
Pfam; PF00027; cMMP_binding; 1.
Pfam; PF00027; cMMP_binding; 1.
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                               777 RGTSRQSLIISMAPSAEGGEEVLTIEVKEKAKQ
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                                                                                                                                                                                                                                  Name=Cngbl; Synonyms=CNG4.3;
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                                                                                                                                                                                                                                                                                          Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                OSS157_RAT PRELIMINARY;
                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
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NUCLEOTIDE SEQUENCE.
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Matches 396;
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777 RGTSROSLIISMAPSAEGGEEVLTIEVKEKAKQ
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01-NOV-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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                                                                                                                                                        Gaps
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
InterPro; IPR005821; Ion Trans.
InterPro; IPR005821; Ion Trans.
InterPro; IPR005821; Ion Trans.
InterPro; ION Trans.
InterPro; ION Trans.
InterPro; ION Trans.
InterPro; IPR00502; ION Trans: 1.
SMART; SM00100; ION Trans: 1.
PROSITE; PS00889; CNMP BINING 1; UNKNOWN 1.
PROSITE; PS00889; CNMP BINING 3; 1.
PROSITE; PS0089; CNMP BINING 3; 1.
SRQUENCE 938 AA; 104518 MW; D1F4FBCF18E53EC4 CRC64;
                                                                                                                                                      Indels
                                                                                                                                  45.3%; Score 1920; DB 2;
.larity 45.9%; Pred. No. 1.9e-103;
Conservative 118; Mismatches 242;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weyand I.; "Cyclic nucleotide-gated channels on the flagellum control Ca2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
MEDLINE-98345361; PubMed-9679145; DOI=10.1083/jcb.142.2.473;
Wiesner B., Weiner J., Middendorff R., Hagen V., Kaupp U.B.,
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PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS0042; CNMP_BINDING_3; 1.
SEQUENCE 948 AA; 105211 MW; 1DA77400115C2074 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cyclic nucleotide-gated channel beta subunit 1d.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.3%; Score 1920; DB 2; 45.9%; Pred. No. 1.9e-103;
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J. Cell Biol. 142:473-484(1998).
EMBL; ARC704013; ARC26128.1; -; mRNA.
HSSP; O88703; 1043.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:006811; P:ion transport; IEA.
InterPro; IPR00695; CNMP. binding.
Pfam; PF00027; CNMP. binding.
Pfam; PF000220; Ion trans.
Pfam; PF000220; Ion trans.
Pfam; PF000220; Ion trans.
Pfam; PF00020; Ion trans.
Pfam; PF00020; Ion trans.
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118; Mismatches 242; Indels 112;
                                                                                ----LSKKNSSGDLTTNPDPQNAAEPTGTVP-----
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                                                                                                                                          ILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLFPPKEETPKLFKTLLGGTGKA
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                 YDGEGNEYLRCYYWAVRTLITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIG
                                 AATANQNYFRACMDDTIAYMNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTV
                                                                                                                          QLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKH
                                                                                                                                                                                   GEVQVLGGPDGTKVLVTLKAGSVFGEI SLLAAGGGNRRTANVVAHGFANLLTLDKKTLQE
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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MEDLINE=98345361; PubMed=9679145; DOI=10.1083/jcb.142.2.473;
Wiesner B., Weiner J., Middendorff R., Hagen V., Kaupp U.B.,
Weyand I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D43F8B1D27F7F052 CRC64;
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08, Last sequence update)
26, Last annotation update)
channel beta subunit le.
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Pred. No. 1.9e-103;
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GO; GO:0002216; F:lon channel activity; IEA.
GO; GO:0006811; P:lon transport; IEA.
InterPro; IPR000595; cNMP_binding.
InterPro; IPR00891; Ion_trans.
Pfem; PF00027; cNMP_binding; 1.
Pfem; PF00027; cNMP_binding; 1.
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PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.

PROSITE; PS00889; CNMP_BINDING_2; 1.

PROSITE; PS50442; CNMP_BINDING_3; 1.

SEQUENCE 952 AA; 105913 MW; D43F8B1D27F7
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J. Cell Biol. 142:473-484(1998).
EMBL; AF074014. AAC26129.1; -; mRNA.
HSSP; O88703; 1Q43.
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  GENNENEQSSRRNEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTPVTSEEPHTN1QDK--
                                                                                                                                   DSRPLIAEENPPSPVQLPLSP--AKSDTLAVPGSATGSLRKRLPSODDEAEELKMLSPAA
                                                                                                                                                                                                                                                                             GDLS----SPEASPQTAKPTAVPPVK--ESDDKPTEHYYRLLWFKVKKMPLTEYLKR1KL
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                                               GAQAQGEVGGAQEQDGVGGA-QDQSTSHQELQ--EEALADSSGVPATEEHPELQVEDADA
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Q28181; Q03861; Q28082;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last sequence update)
240 kDa protein of rod photoreceptor CNV-channel (Contains: Glutaicid-rich protein (GARP); Cyclic-nucleotide-gated cation channel (CNG channel 4) (CNG-Channel CNG Channel 4) (CNG-Channel CNG Channel 4)
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Extracellular (Potential)

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R InterPro; IPR00595; NMP bd.

InterPro; IPR00595; NMP bd.

InterPro; IPR00595; NMP bd.

R Pfam; PF006207; NMP binding; 1.

R Pfam; PF006207; NMP BINDING 1; 1.

R PROSITE; PS00889; CMMP BINDING 2; 1.

R PROSITE; PS00899; CMMP BINDING 2; 1.

R PROSITE; PS0089; CMP binding; 1.

R Alternative splicing; CAMP; CAMP-binding; Direct protein sequencing; M Glycoprotein; Ion transport; Ionic channel; Multigene family; CHAIN 454 1394 CYPlic-nucleoxide-gated cation channel 4.

TOPO DOM 1 770 Cytoplasmic (Potential).
                                                                                                                           NUCLECTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
MEDLINE=96099859; PubMed=7546742; DOI=10.1016/0896-6273(95)90151-5;
Koerschen H.G., Illing M., Seifert R., Sesti F., Williams A.,
Gotzes S., Colville C., Mueller F., Dose A., Godde M., Molday L.,
Kaupp U.B., Molday R.S.;
M. 240 kDa protein represents the complete beta subunit of the cyclic nucleotide-gated channel from rod photoreceptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=026181-3; Sequence=VSP_001108;
-1- TISSUE SPECIFICITY: Retina, testis, kidney, heart and brain.
-1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
-1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Retina;
PubMed=2014230;
Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;
Sugimoto Y., Vatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;
"The amino acid sequence of a glutamic acid-rich protein from bovine
retina as deduced from the cDNA sequence.";
Proc. Natl. Acad. Sci. U.S.A. 88:3116-3119(1991).
-!- SUBUNIT: Forms functional heterooligomeric channels with CNG3.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glutamic acid-rich protein.
Cyclic-nucleotide-gated cation channel
Cytoplasmic (Potential).
HI (Potential).
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Modecular cloning and expression of the modulatory subunit of the
cyclic nucleotide-gated cation channel.";
J. Biol. Chem. 271:6349-6355(1996).
               Name=CNGB1; Synonyms=CNCG4;
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 454-1394 (ISOFORMS CNG4C; CNG4D AND CNG4E)
                                                                                                                                                                                                                                                                                           TISSUE=Testis;
MEDLINE=96198098; PubMed=8626431; DOI=10.1074/jbc.271.11.6349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=3;
Comment=Isoform CNG4D is the most frequent isoform
(CNG4D:CNG4C:CNG4E = 20:2:1) in testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=028181-2; Sequence=VSP_001109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q28181-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X89626; CAA61769.1; -; MRNA.
EMBL; X94707; CAA64367.1; -; MRNA.
EMBL; M61185; AAA30536.1; -; MRNA.
                                                                                  Pecora; Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 1-590.
subunit)]
                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=CNG4E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=CNG4D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=CNG4C
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THE LAKE WAS DEPARTED BY A COURT OF COURT OF STANKING AND A COURT OF STANKING

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999 AATAGGIYYRSCMDSTVKYMNFYKIPRSVONRVKTWYEYTWHSOGMLDESELMVOLPDKM 1058
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                                                                                                                                                                                                                                                                                                  cAMP (Potential).
N-linked (GlcNAc. .) (Potential).
Missing (in isoform CNG4E).
/FTIG-VSP 001108.
/FTIG-VSP_001109.
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A -> T (in Ref. 3).
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S -> A (in Ref. 2).
R -> A (in Ref. 2).
D -> E (in Ref. 2).
A -> AA (in Ref. 2).
A -> AA (in Ref. 2).
MW; EEGDAS59BE3744A7 CRC64;
                                         H3 (Forential).

Extracellular (Potential).

Cytoplasmic (Potential).

H5 (Potential).

Extracellular (Potential).

H6 (Potential).
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cAMP (By similarity).
cAMP (Potential).
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(Potential)
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Matches 326;
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Cattelli V., Retinka M., Vacherie B.,
Biemont C., Skalli Z., Cattellio L., Poulain J., De Berardinis V.,
A michouard V., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                   1280
                          1281 SASPEQPPRPEPPAPEAPAPEPTAPEPLAPEAPAPEAPASSPPPASQERPEGDKDAARP 1340
  RLDLAIDVNYSIVSKVALFQGCDRQMIFDMLKRLRSVVYLPNDYVCKKGEIGREMYIIQA 1118
                                                                                                                                        734
                                                                                                                                         687 SL------ARLLKLKREQAAQKKENSEGGEEEGKENEDKQKENEDKG
                                                                                                                                                                   1233 GAKGGRGGRLALLRARLKELAALEAARQQQL---LEQAKSSEDAAVGEE-----G
                                                                                                                                                                                               735 KENEDKDKGREPEEKPLDRPECTA------SPIAVEEEPHSVRRTVLP
                                                                                 ILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLFPPKEETPKLFKTLLGGTGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14565, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope, Whitehead Institute Centre for Genome Research, Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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EMBL; CARADO1014565; CRMP B023.1; -; Genomic_DNA.
InterPro; IPR00595; CNMP bd.
InterPro; IPR00595; Ion_Trans.
Pfam; PF00027; CNMP binding; 1.
Pfam; PF00027; CNMP binding; 1.
Pfam; PF000520; Ion_trans; 1.
SMART; SM00100; CNMP; 1.
PROSITE; PS000899; CNMP BINDING 1; UNKNOWN 1.
PROSITE; PS000899; CNMP BINDING 2; UNKNOWN 1.
PROSITE; PS00042; CNMP_BINDING 3; 1.
                                                                                                                                                                                                                                                                     777 RGTSRQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809
                                                                                                                                                                                                                                                                                                                                                      573 AA
                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
ORFNames=GSTENG00016673001;
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Q4SKK9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 431:946-957(2004)
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                                                                                                                                                                                                                                                                                                                                                                                                            296 TSTKFQ-LDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 RTTGYLLFILHINACVYYWASNYEGIGTTRWVYDGEGNEYLRCYYWAVRTLITIGGLPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 QTLFEIVFQLLNFFSGVFVFSSLIGOMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOKRVRTWYEYTWDSQRML------DESDLLKTLPTTVQLALAIDVNFSIISKVDLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKA
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                                                                                                                                                                                                                                                                                                                 178 DKPTEHYYRLLWFKVKKM--PLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLAYNWNCWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetrandon nigrovizidas (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Neoteleostomi;

Actinopterygii, Neopterygii, Taleostei, Euteleostei; Neoteleostei;

Acanthomorpha, Acanthopterygii, Percomorpha; Tetraodontiformes;

Tetradontoidea, Tetraodonidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF9565, whole genome shotgun sequence.
                                                                                                                                         19;
                                                                                            38.7%; Score 1639.5; DB 2; Length 56.4%; Pred. No. 2.3e-87;
                                                                                                                                         84; Mismatches 149; Indels
1 1
573 573
573 AA, 64995 MW, 942B58B39B630BB9 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last seq
13-SEP-2005 (TrEMBLrel. 31, Last ann
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                                                                                                                                            Conservative
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                                                                                                                     Similarity
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Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,

Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

Nature 431:946-957(2004).

Nature 431:946-957(2004).

ROUGLEOTIDE SEQUENCE.

Genoscope, Whitchead Institute Centre for Genome Research;

Genoscope, Whitchead Institute Centre for Genome Research;

Submitted (FRB-2004) to the EMBL/Genbank/DDBJ databases.

C.: CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KMPLTEYLKRI----KLPNSIDSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQTA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDRKEMRENYMTTDRFKTDLLSLFPLELCYIFTGVNPLLRFPRLLKYQVFFFFNDRMEAV 304
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                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.

EMBL, CAAE0109565; CAF22127.1; -; Genomic_DNA.

InterPro; IPR005821; Ion_trans.

Pfam, PF00520; Ion_trans.

Ion_transport; Ionic channel; Transmembrane; Transport.
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743 AA; 83811 MW; 27350BFD6A8D226D CRC64;
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SEQUENCE
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Search completed: December 21, 2005, 19:58:05 Job time: 238 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein December 21, 2005, 19:46:13; Search time 186 Seconds (without alignments) 1911.061 Million cell updates/sec Run on:

US-09-855-828-1

4234 1 MFKSLTKVNKVKPIGENNEN......PSAEGGEEVLTIEVKEKAKQ 809 score: Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 Total number of hits satisfying chosen parameters: 2443163 segs, 439378781 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_21:* Database :

Genesequi 980s:*
genesequi 990s:*
genesequi 990s:*
genesequi 2000s:*
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genesequi 2003s:*
genesequi 2003s:*
genesequi 9003bs:*
genesequi 9003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aae15982 Human cyc	Aae15983 Human CNC	Aae15985 Human CNC	Aae15984 Human CNG	Aae15986 Human CNG	Adz88289 Human CNG	_	Aeal7267 Human cy	Abm83979 Human dia	Novel	Abb66545 Drosophi	Abg05466 Novel hun	Adz88294 Human CNC	Abg11969 Novel hum	Abr39396 Amino aci	Abp98584 Amino aci	Aae15987 Human CNG	Aae38591 Human CNC	Adz88286 Human CNC	Add48638 Rat Prote	Aag79527 Cow HBMY(a	Adz88292 Bull CNG	Ado67650 Novel hum
ΙD	AAE15982	AAE15983	AAE15985	AAE15984	AAE15986	ADZ88289	ADZ88287	AEA17267	ABM83979	ABG27471	ABB66545	ABG05466	ADZ88294	ABG11969	ABR39396	ABP98584	AAE15987	AAE38591	ADZ88286	ADD48638	AAG79527	ABG74912	ADZ88292	AD067650
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% Query Match	100.0	66.66	99.9	99.9	99.9	76.0	46.1	46.0	46.0	42.1	26.1	25.7	24.9	22.6	21.4	21.3	20.1	20.1	20.1	19.6	19.6	19.6	19.6	19.5
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Aag79525 Variant H Abg74914 Bovine CN Abg74913 Bovine CN Abg72530 Novel hum		Abb78066 Amino aci Abg72529 Novel hum Abu12049 Human NOV Abp98475 Amino aci		Adr09903 Human Pro Adr09903 Human pro Aae15988 Human CNG Adz88293 CNG chann Aag79529 Rat HBMYC
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ALIGNMENTS

Human cyclic nucleotide-gated cation channel 3 beta subunit protein. AAE15982 standard; protein; 809 AA (first entry) 26-MAR-2002 AAE15982; RESULT 1 AAE15982

Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B; cyclic nucleotide-gated ion channel; contraceptive; vision disorder; male infertility; genetic defect; reporter-ligand interaction; CNG; viral infection; cancer.

Homo sapiens

210. .661 /note= "Conserved region; this region also function as an epitope and is referred in claim 1" Location/Qualifiers 15-MAY-2001; 2001WO-US015814 WO200188090-A2. 22-NOV-2001. Key Region

15-MAY-2000; 2000US-0204445P. 14-MAY-2001; 2001US-00855828. Creech CD, Jegla TJ; WPI; 2002-089847/12. N-PSDB; AAD25729. (ICAG-) ICAGEN INC.

New polypeptide, useful for screening for modulators of cyclic nucleotide -gated ion channels, comprises the isolated cyclic nucleotide-gated cation channel 3 beta subunit.

Claim 12; Fig 4; 83pp; English.

The invention relates to human cyclic nucleotide-gated cation channel 3 beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms

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functional heteromultimers with CNGA1 and/or CNGA3, two CNG alpha subunits that are expressed in retina. CNG3B polypeptides are useful for screening modulators of CNG9 which are useful as contraceptives and retina treating various disorders involving cation channels, e.g. vision disorders and male infertility. Polynucleotides of the invention are useful for transfection of cells in vitro and in vivo, to correct acquired and inherited genetic defects, cancer and viral infections. Sequences of the invention are useful as reporter molecules in assays and detection systems, to measure changes in cation concentration, membrane potential, current flow, ion flux, transcription, signal transduction, reporter-ligand interactions and second messenger concentrations, in viro and ex vivo. They are useful to construct models of CNGs in a computer system and for examining expression and regulation of cation channels. The present sequence is human CNG3B protein
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The invention relates to human cyclic nucleotide-gated cation channel 3 beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a membra of cyclic nucleotide-gated cation channel (CNG) family. CNG3B is a membra of cyclic nucleide-gated cation channel (CNG) family. CNG3B polyments from the commitmers with CNG3A and/or CNGA3, two CNG alpha subunits that are expressed in retina. CNG3B polypeptides are useful for sortening modulators of CNGs which are useful as contraceptives and for treating various disorders involving cation channels, e.g. vision disorders and male infertility. Polynucleotides of the invention are useful as reporter molecules in insays and acquired and inherited genetic defects, cancer and viral infections. Sequences of the invention are useful as reporter molecules in assays and effection systems, to measure changes in cation concentration, membrane potential, current flow, ion flux, transcription, signal transduction, viro, in vivo and ex vivo. They are useful to construct models of CNGs in a computer system and for examining expression and regulation of cation channels. The present sequence is human CNG3B protein variant (R142K). Note: This sequence is not shown in the specification, but is derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig
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The invention relates to human cyclic nucleotide-gated cation channel 3 beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member of cyclic nucleotide-gated cation channel (CNG) family. CNG3B is a member functional heteromultimers with CNGA1 and/or CNGA1, two CNG 3D forms subunits that are expressed in retina. CNG3B polypeptides are useful for screening modulators of CNGS which are useful as contraceptives and for treating various disorders involving cation channels, e.g. vision disorders and male infertility. Polynucleotides of the invention are useful for transfection of cells in vitro and in vivo. to correct useful contract and inherited genetic defects, cancer and viral infections. Sequences of the invention are useful as reporter molecules in assays and detection systems, to measure changes in cation concentration, membrane potential, current flow, ion flux, transcription, signal transduction, reporter-ligand interactions and second messenger concentrations.
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Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B; cyclic nucleotide-gated ion channel; contraceptive; vision disorder; male infertility; genetic defect; reporter-ligand interaction; CNG; viral infection; cancer; mutant; mutehn; variant.
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The invention relates to human cyclic nucleotide gated cation channel to beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms functional heteromultimers with CNGA1 and/or CNGA3, two CNG alpha subunits that are expressed in retina. CNG3B polypeptides are useful for screening modulators of CNG8 which are useful as contraceptives and for treating various disorders involving cation channels, e.g. vision disorders and male infertility. Polynucleotides of the invention are useful for transfection of cells in vitro and in vivo, to correct acquired and inherited genetic defects, cancer and viral infections. Sequences of the invention are useful as reporter molecules in assays and detection systems, to measure changes in cation concentration, membrane potential, current flow, ion flux, transcription, signal transduction, reporter-ligand interactions and second messenger concentrations, in vivo and ex vivo. They are useful to construct models of CNGs vitro, in vivo and ex vivo. They are useful to construct models of
                                                                          New polypeptide, useful for screening for modulators of cyclic nucleoride eated ion channels, comprises the isolated cyclic nucleoride quind cation channel 3 beta subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in a computer system and for examining expression and regulation of cation channels. The present sequence is human CNG3B protein variant (D154N). Note: This sequence is not shown in the specification, but is derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig 4 of the specification (AAE15982)
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          DLALLFPPKEETPKLFKTLLGGTGKASLARLKKKREQAAQKKENSEGGEEEGKENEDKQ
                                                                                                                           GNRRTANVVAHGFANLLTLDKKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRK
                                                                           DLALLPPPKEETPKLFKTLLGGTGKASLARLLKLKREQAAQKKENSEGGEEGKENEDKQ
KSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGG
                                                  GNRRTANVVAHGFANLLTLDKKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRK
                                                                                                                 KENEDKOKENEDKGKENEDKDKGREPEEKPLDRPECTASPIAVEEEPHSVRRTVLPRGTS
                                                                                                                                                                                                                                                                                                     Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B; cyclic nucleotide-gated ion channel; contraceptive; vision disorder; male infertility; genetic defect; reporter-ligand interaction; CNG; viral infection; cancer; mutant; mutein; variant.
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2001US-00855828.
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14-MAY-2001;
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acquired and inherited genetic defects, cancer and viral infections. Sequences of the invention are useful as reporter molecules in assays and detection systems, to measure changes in cation concentration, membrane potential, current flow, ion flux, transcription, signal transduction, reporter-ligand interactions and second messenger concentrations, in viro, in vivo and ex vivo. They are useful to construct models of CNGs in a computer system and for examining expression and regulation of cation channels. The present sequence is human CNG3B protein variant (GRB2S). Note: This sequence is not shown in the specification, but is derived from the human wild type CNG3B protein (SEO ID NO:1) shown in Fig 4 of the specification (AAE15982)
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Best Local Similarity 99.9%;
Matches 808; Conservative
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Antiparkinsonian; Antidepressant; Neuroleptic; Cardiant; GPCR-Antagonist; Unspecified GPCR; cyclic nucleotide-gated channel A2; CNGA2; CNG; mutation; divalent cation-mediated blockage; cation flux; G-protein coupled receptor; astchma; hypertension; allergic reaction; Parkinsons disease; depression; schizophrenia; heart disease.
                                                                                                                                                                                                                                                                                                   antiasthmatic; Antiallergic; Hypotensive; Gastrointestinal-Gen.;
                                                           ADZ88289 standard; protein; 615 AA
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20-JUL-2004; 2004US-0589012P.
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                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                               Human CNG channel CNGB3
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RESULT 6

ADZ288289

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This sequence represents a wild type human cyclic nucleotide-gated (CNG) channel. The rat CNG channel sequence, CNGA2, may be mutated to form the invention which comprising a sequence concoding a mutant CNG channel comprising at least one mutation that decreases divatent cation-mediated blockage of cation flux, and at least one mutation that makes the channel more sensitive to cAMP than a channel that decenting changes in intracellular levels of CAMP, comprising expressing in a cell the polymucleotide cited above, and measuring cativity of the channel, where activity of the channel, is indicative of changes in intracellular cAMP; (D) detecting activity of a GPCR, comprising expressing the CNG channel and the G-protein coupled receptor (GPCR) in host cell transformed with the nucleotide of the invention, and measuring activity of the Channel, where activity of the channel coupled receptor (GPCR) in host cell transformed with the nucleotide of the invention, and comprising contacting a cell with a compound wherein the call expresses that the compound is a ligand for the creeptor and the mutant CNG channel cited above, and measuring activity of the CNG channel cited above, and measuring activation of the CNG channel, where activation of the CNG channel contacting the transformed host cell with the agent and a ligand for the receptor, and measuring activation of the CNG channel. The methods and contacting the transformed host cell with the agent and a ligand for the receptor, and measuring activation of the CNG channel. The methods and contacting the transformed host cell with the agent and a ligand for the receptor, and measuring activation of the CNG channel. The methods and contacting the transformed host cell with the agent and a ligand for the receptor, and measuring activation of the CNG channel. The methods and contacting the transformed host cell with the agent and a ligand for the receptor, and measuring activation of the CNG channel and was and other indicators, including novel CNG mutants for cell-based 
New isolated polynucleotide encoding a mutant cyclic nucleotide-gated (CNG) channel having a mutation that decreases divalent cation-mediated blockage of cation flux, and makes the channel more sensitive to cAMP.
                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 14; 156pp; English
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12-MAY-2005

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Antiparkinsonian; Antidepressant; Neuroleptic; Cardiant; GPCR-Antagonist; Unspecified GPCR; cyclic nucleotide-gated channel A2; CNGA2; CNG; mutation; divalent cation-mediated blockage; cation flux; G-protein coupled receptor; asthma; hypertension; allergic reaction; Parkinsons disease; depression; schizophrenia; heart disease.
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                                          Similarity
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053 KKDLNEILVHYPESQKLLRKKARRMLRSNNK-----PKEEKSVLILPPRAGTPKLFNAAL 1107
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                                                  DIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFGFN 320
                                                                                                                                                                                                                                                                                                                                                             MRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLK 500
----QFPQSIDPLTNLMYVLWLFFVVMAWNWCWLIPVRWAFPYQTPDNIHHWLLMDYLC 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLIYFLDITVFQTRLQFVRGGDIITDKKDMRNNYLKSRRFKMDLLSLLPLDFLYLKVGVN
                                                                                                                                                                                GTTRWVYDGEGNEYLRCYYWAVRTLITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGGGNRRTANVVAHGFANLLTLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLFPPKEETPKLFKTLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501 TLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKE
                                                                                                                                                          PMFRANRMLKYTSFFBFNHHLESIMDKAYIYRVIRTTGYLLF1LHINACVYYWASNYEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cyclic nucleotide gated cation channel 4 (CNG) protein SEO ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ICMSPGPEPGEQILSVKMPEEREE 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      777 RGTSRQSLIISMAPSAEGGEEVLTIEVKEKAKO 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 screening; cyclic adenosine monophosphate; cyclic nucleotide gated cation channel 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEA17267 standard; protein; 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-NOV-2003; 2003EP-00027311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     channel. The rat CNG channel sequence, CNGA2, may be mutated to form the isolated polynucleotide of the invention which comprising a sequence concoting a mutation that according a mutation that decreases divalent cation-mediated blockage of cation flux, and at least one mutation that makes the channel comprising at least one mutation that makes the channel more sensitive to cAMP than a channel comprise the mutation. The invention includes methods for:

(a) detecting changes in intracellular levels of cAMP, comprising expressing in a cell the polynucleotide cited above, and measuring cativity of the channel, where activity of the channel, where activity of the channel and the G-protein coupled receptor changes in intracellular cAMP; (b) detecting activity of a GPCR, comprising activity of the channel and the G-protein coupled receptor (GPCR) in host cell transformed with the nucleotide of the invention, and indicates activity of the GPCR; (c) identifying of the channel compound wherein the cell expresses the receptor and the mutant CNG channel cited above, and measuring activity of the GPCR; (c) identifying of the cransformed host cell with a compound wherein the coll expresses contacting the transformed host cell with the agent and a ligand for the receptor; and measuring activity mediated by a GPCR, comprising contacting the transformed host cell with the agent and a ligand for the receptor; and measuring activation of the CNG channel, the methods and compositions of the present invention are useful in cellular physiology, in particular for cell-based assays that employ calcium and voltage-based dyes and other indicators, including novel CNG channel and hast cell was a such as such as a such as a sham, hypertension, allergic reactioning and hast reactive expective chicked and experienced the activity of GPCR in disorders and down allergic measuring the activity of GPCR in disorders and down and an activity of solid contactine assays, and for measuring the activity of GPCR in disorders and experience.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- VINEYADAQLHNLVKRMRQRTALY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 LKRIKLPNSIDSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQTADNIHYWLIADIIC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders, Parkinson's disease, depression, schizophrenia and heart
disease. This sequence was included in the specification for comparison
                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide encoding a mutant cyclic nucleotide-gated (CNG) channel having a mutation that decreases divalent cation-mediated blockage of cation flux, and makes the channel more sensitive to CAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a wild type human cyclic nucleotide-gated (CNG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGEBAKKEABEKAKEEAEBVAEBEAEKEPODWAETKEEPEAEAEASSGVPATKOHPEVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 IGENNENEQSSRRNEEGSHPSNQSQQTTAQE--ENKGE---EKSLKTKSTPVTSEEPHTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 IQDK-----LSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 46.1%; Score 1952; DB 9; Local Similarity 46.4%; Pred. No. 8.2e-157; les 405; Conservative 121; Mismatches 237;
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 12; 156pp; English.
                                                                                                                                                                                                                  Llorente I;
                                  01-NOV-2004; 2004WO-US036022
                                                                                     30-OCT-2003; 2003US-0515442P.
20-JUL-2004; 2004US-0589012P.
                                                                                                                                                             BIOSCIENCE INC.
                                                                                                                                                                                                                  Lu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SPONKP---
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                                                                                                                                                                                                                  Cao L,
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The invention relates to a chimeric peptide (I) for direct determination of CAMP concentration in vitro and/or in vivo. (I) comprises: (a) a cAMP binding givoup having only one CAMP binding give (b) at least two detectable labels is least two detectable labels, where a first of the two detectable labels is located at the amino terminus of the cAMP binding group of (a). Also concentration (II) a noncious of the cAMP binding group of (a). Also concerted (1) a nucleic acid molecule (II) encoding (II) (2) a vector (III) comprising (II); (3) a host (IV) transformed with (III) or transfected with (III); (4) producing (MI) the chimeric peptide comprising culturing/raising (IV) and optionally, isolating and/or purifying the produced chimeric peptide; and (5) a kit comprising any one of (I)-(IV), or or organs or calls of a non-human transgenic animal of (IV), (I) is useful for determining the concentration of cAMP in a sample, which involves adding (I), or (IV) to the sample, and measuring/recording fluorescence energy transfer (FRET) or bioluminescence concentration in the sample by comparing values of the fluorescence emission with a cresonance energy transfer (BRET) and determining cAMP concentration in the sample by comparing values of the fluorescence emission with a comparing values of the fluorescence emission with a concentration of cAMP in a living cell or a concentration of cAMP in a living cell or a mount/distribution/location/fluctuation of cAMP in a living cell or a condicate animal of (IV) or organs or cells of concentration cells of concentration of camp signaling in the present concentration of the present invention.

Congenesis or pathogenesis of diseases of an organ. The present congeneration of the present invention. --SPONKP-----PAAP------PAAP-------VINEYADAQLHNLVKRMRQRTALY 146 185 ALSPAESPVVAWSDPTTPKDTDGQDRAASTASTNSAIIND----RLQELVKLFKERTEKV 240 241 KEKLIDPDVTSDEESPKPSPAKKAPEPAPDTKPABAEPVEEEHYCDMLCCKFKHRPWKKY 300 260 DIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFGFN 320 PMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACVYYWASNYEGI 380 14 IGENNENEQSSRRNEEGSHPSNQSQQTTAQE -- ENKGE--- EKSLKTKSTPVTSEEPHTN 201 LKRIKLPNSIDSYTDRLYLLWILLVTLAYNWNCWFIPLRLVFPYQTADNIHYWLIADIIC KKKLVEGDLS----SPEASPQTAKPTAVPPVKESDDKPT--EHYYRLLWFKVKKMPLTEY Indels 110; 69 IODK-----LSKKNSSGDLTTNPDPONAAEPTGTVPEQKEMDPGKEGPN-Length 909; Local Similarity 46.2%; Pred. No. 9.2e-157; es 403; Conservative 122; Mismatches 238; 46.0%; Score 1949; DB 9; 46.2%; Pred. No. 9.2e-157; SEQ ID NO 5; 103pp; English. Sequence 909 AA; Query Match 113 147 301 261 357 321 417 ઠે 셤 ò 셤 δ g B & ઠે ద ò ద કે g

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 272 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may but Ω; Gietzen New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy in gene mapping. TLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKE 597 QLPDKMRLDLAIDVNYNIVSKVALFQGCDRQMIFDMLKRLRSVVYLPNDYVCKKGEIGRE 657 MYIIQAGQVQVLGGPDGKSVLVTLKAGSVFGBISLLAVGGGNRRTANVVAHGFTNLF1LD KKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLFPPKEETPKLFKTLL 681 GGTGKAS-----LARLLKLKREQAAQKKENSEGGEEEGKENEDKQKENEDKQK 772 AMTGKMGGKGAKGGKLAHLRARLKELAALEAAAKHEEL----VEQAKSSQDVKGEEGSAAP Kirton ES; gene therapy; human diagnostic and therapeutic polynucleotide; dithp. Gerstin EH; Wright RJ, Bruns CM, Marjanovic MM, Shen F;
TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Spric PA, Stewart EA, Wingrove J, Vitt UA, Kirton SM, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gie Shi X, Suarez CJ; : DQHTHPKEAATDPPAPRTPPEPP-GSPPSSPPPASLGSCEGEEGPAEPERSVR Human diagnostic and therapeutic pprotein SEQ ID NO:4228 ENEDKGKE-NEDKDKGREPEEKPLDRPECTASPIAV----777 RGTSRQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809 -----ICMSPGPEPGEQILSVKMPEEREE ABM83979 standard; protein; 1250 Claim 27; Page; 190pp; English 12-SEP-2002; 2002US-0410259P. 12-SEP-2003; 2003WO-US028227 (INCY-) INCYTE CORP. 2004-329368/30 Kwong M, Po WPI; 2004-329368/ N-PSDB; ACN42631. WO2004023973-A2. 18-NOV-2004 Harthshorne 25-MAR-2004. Stevens KA, Peralta CH, Schmidt JP, Mooney EM, Lagace RE, 501 717 729 621 ABM83979 ઠે 유 ò 셤 à g ò g ò 엄

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KDLNEILVHYPESQKILRKKARRMIRSNNK----PKEEKSVLILPPRAGTPKIFNAALA 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     999 YIIQAGQVQVLGGPDGKSVLVTLKAGSVFGEISLLAVGGGNRRTANVVAHGFTNLFILDK 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         681
       with human molecules, e.g. cell proliferative disorders, autoimmune/Inflammatory disorder, developmental disorders, endocrine disorder, neurological disorders, developmental disorders, endocrine infections caused by virus, bacteria, fungi or parasite. The diths molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence date for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGKAS------LARLLKLKREQAAQKKENSEGGEEGKENEDKQKEN729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  758
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                                                                                                                                                                                                                                                                                                                                                                VGEEAKKEAEEKAKEEAEEVAEEBAEKEPQDWAETKEEPEAEAAASSGVPATKQHPEVQ 468
                                                                                                                                                                                                                                                                                                                                                                                                   IQDK-----LSKKNSSGDLTTNPDPQNAAEPTGTVP---------ESKK 103
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disease or disorder associated
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                                                                                                                                                                                                                                                       Query Match 46.0%; Score 1948.5; DB 8; Length 1250; Best Local Similarity 46.2%; Pred. No. 1.6e-156; Matches 403; Conservative 125; Mismatches 235; Indels 109;
                                                                                                                                                                                                                                                                                                                                14 IGENNENEQSSRRNEEGSHPSNOSQQTTAQE--ENKGE-
particular condition,
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                                                                                                                                                                                                                          Sequence 1250 AA;
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reaction (PCR) primers, oligomers, and for chromosome and gene mapping, reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclecuides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cetivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food involving aberrant protein expression or biological activity. The involving aberrant protein expression or biological activity. The diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity.
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1171 QHTHPKEAATDPPAPRTPPEPPGSPPSSPPPASLGRPEGEEGGPA-EPEEHSVR----- 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to isolated polynucleotide (1) and polypeptide (11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                  forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47:
                                                                                                                                                                                                                                                                                                                Human, chromosome mapping; gene mapping; gene therapy, forensic
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                           Claim 20; SEQ ID NO 57830; 103pp; English.
                                    778 GTSRQSLIISMAPSAEGGEEVLTIEVKEKAKQ
                                                                                                                                                                                                                                                                              Novel human diagnostic protein #27462.
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                                                                                                                                                                  ABG27471 standard; protein; 652
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23-AUG-2000; 2000US-00649167.
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Matches 343;
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AQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPVKESDDKPTEHYYRLLW 189
                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidaring cell signalling and call-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDKLSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPAAPVINEYAD
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                                                            New isolated nucleic acid detection reagent for detecting 1000 or genes from Drosophila and for elucidating cell signaling and cell interactions.
                                                                                                                                            + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
26.1%; Score 1103; DB 4; Length 1
Best Local Similarity 33.4%; Pred. No. 2.1e-84;
Matches 243; Conservative 153; Mismatches 255; Indels
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                                                                                                                                            Disclosure; SEQ ID NO
  WPI; 2001-656860/75.
N-PSDB; ABL10648.
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VNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLG
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                                                                                                                                                             FFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACVYYWASNYEGIGTTRWVYDGEGNE
                                                                               RLOFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFGFNPMFRANRMLKYTS
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pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 26427
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                 1; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 35825; 103pp; English.
                                                                                                                                                                                                                                                            Novel human diagnostic protein #5457.
                                                                                                                                         ABG05466 standard; protein; 644 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
AOKKENS
                                     MRRKROS
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                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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antiasthmatic; Antiallergic; Hypotensive; Gastrointestinal-Gen.; Antiparkinsonian; Antidepressant; Neuroleptic; Cardiant; GPCR-Antagonist; Unspecified GPCR, cyclic nucleotide-gated channel A2; CNGA2; CNG; mutation; divalent cation-mediated by Cockage; cation flux; G-protein coupled receptor; astehma; hypertension; allergic reaction; Parkinsons disease; depression; schizophrenia; heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a consensus sequence of the human cyclic nucleotide-gated (CNG) channel proteins, CNGA1 - CNGA3 and CNGB1 - CNGB3. The rat CNG channel sequence, CNGA2, may be mutated to form the isolated polynucleotide of the invention which comprising a sequence encoding a mutant CNG channel comprising at least one mutation that decreases mutation comprise the channel more sensitive to cAMP than a channel that does not comprise the mutation. The invention includes methods for: (a) detecting changes in intracellular levels of cAMP, comprising expressing in a cell the polynucleotide cited above, and measuring activity of the channel, where activity of the channel is indicative of changes in intracellular cAMP; (b) detecting activity of a GPCR,
713
                                                                       773
                                                                                          New isolated polynucleotide encoding a mutant cyclic nucleotide-gated (CNG) channel having a mutation that decreases divalent cation-mediated blockage of cation flux, and makes the channel more sensitive to cAMP.
                   BATPPRKDLALLFPPKEETPKLFKTLLGGTGKASLARLLKLKREQAAQKKENSEGGEEEG
EATPPRKDLALLFPPKEETPKLFKTLLGGTGKASLARLLKLKREQAAQKKENSEGGEEEG
                                                                       KENEDKOKENEDKOKENEDKGKENEDKDKGREPEEKPLDRPECTASPIAVEEEPHSVRRT
                                                                                                                                                                                    644
                                                                                                                                                                                                                                                                                                                                                                                             Human CNG channel proteins consensus sequence.
                                                                                                                                                774 VLPRGTSROSLIISMAPSAEGGEEVLTIEVKEKAKO
                                                                                                                                                                                    609 VLPRGTSRQSLIISMAPSAEGGEEVLTIEVKEKAKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, SEQ ID NO 19; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                               ADZ88294 standard; protein; 821 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Llorente I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2004; 2004WO-US036022
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20-JUL-2004; 2004US-0589012P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ATTO-) ATTO BIOSCIENCE INC.
                                                                                                                                                                                                                                                                                                                                                      (first entry)
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ID ADZ
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25.7%; Score 1088; DB 4; Length 644; 100.0%; Pred. No. 2e-83; cive 0; Mismatches 0; Indels (

Conservative

Matches 216;

Local Similarity

Query Match

Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.

30-MAR-2001; 2001WO-US008631.

WO200175067-A2

11-OCT-2001

Homo sapiens.

Novel human diagnostic protein #11960.

18-FEB-2002

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GGPCR) in host cell transformed with the nucleotide of the invention, and measuring activity of the channel, where activity of the channel indicates activity of the Channel, where activity of the channel compound wherein the cell expresses comprising contacting a cell with a compound wherein the cell expresses the receptor and the mutant CNG channel cited above, and measuring activation of the CNG channel, where activation of the CNG channel cited above, and measuring activation of the CNG channel is a ligand for the receptor; (d) identifying a agent that modulates an activity mediated by a GPCR, comprising contacting the transformed host cell where cNG channel. The methods and creeptor, and measuring activation of the CNG channel. The methods and compositions of the present invention are useful in cellular physiology, in particular for cell-based assays that employ calcium and voltage-based dyes and other indicators, including novel CNG mutants for cyclic compositions of the measuring the activity of GPCR in disorders such as asthma, hypertension, allergic reactions, gastrointestinal cliented assays. This sequence was included in the specification for comparison
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 expressing the CNG channel and the G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLPNSIDSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                                                                                                                                     24.9%; Score 1052.5; DB 9; Length 821; 38.6%; Pred. No. 3.1e-80; ive 97; Mismatches 205; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGEEGKENEDKQKENEDKQKENEDKGKENEDKDKGREPEEKPLDRPE 755
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Matches 227; Conservative
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 comprising
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) as useful in gene therapy techniques to restore normal cativity of (II) as useful for generating antibodies against it, detecting or quantitating useful for generating antibodies against it, detecting or quantitating oblypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.6%; Score 955; DB 4; 32.8%; Pred. No. 5.7e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 42328; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                 Tang YT;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
N-PSDB; AAS76156.
                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
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ABG11969 standard; protein; 747 AA.

RESULT 14

ABG11969;

ABG11969 ID ABG1 XX AC ABG1

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343
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                                                                                          344 LGSGETTKPRNSGSTGRRKESKQLKAGSQREWLQVQIQTIGILMSEKAELWTALYYTQHA 403
                                                                                                                                                                       464 IMONDLITISHAVFONGELKEQLAKLOTGFMKLNNENMEITSTPOSEQHIKKEPSEKLGD 523
                                                                                                                                                                                               --FNH 339
                                                                                                                                                                                                                  583
                                                                                                                                                                                                                                       340 HLESIMDKAYIYR------ 352
                                                                                                                                                                                                                                                          584 FMELMQEKVDLKEQMEKLERRCIQLSGETDVIIHHTVPELEVSAEDVAPEGIHQQPGPGQ 643
                                                                                                                                                                                                                                                                                                   644 GGDEGEAAGAAGAAGAGGIPEEGIVIIGNDSSTHVMEPEDLPVGQDVDVEDSDIDDP 703
SFSPIWFVDCDDPNLTSVLERPEDTENNNYIRQQLKCTWMFEMLDQPLPMGQNGKIEVTS 283
                                                                                                                                   404 ARQFEGESKDLASCLQYSWRVQDNEGLSLLNREQEERLLELEQKAELWEEQVEVHRQTLE 463
                                                 284 EEEEEEMAGDIKYLNHCKMKKEELISGKKLEDEGIEKENLATLEKIRKTQSQGHLNVMMC
                                                                                                                                                      ----DICYLFFGFNPMFRANRMLKYTSFFE--------
                                                                                                                                                                                                                 524 GLDSEEEALPLMPSIPEELESREAMVAFLNSAVASAEEEQAWPRGQLKEQRGAMEKLQSH
                                                                                                                                                                                                                                                                                                                     OCNCI; OCNC2; betalb; CNG; human; olfactory cyclic nucleotide gated channel subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of human betalb
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                                                                                                               -----DVASIIPF-----
                                                                                                                                                                                                                                                                                                                                                                                               ABR39396 standard; protein; 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-2001; 2001US-0303140P.
10-DEC-2001; 2001US-0337154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SENO-) SENOMYX INC
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The present invention relates to a nucleotide sequences encoding human CONCI, OCNC2, or betalb olfactory cyclic nucleotide gated (CNG) channel subbunit, its action being an olfactory CNG channel activity modulator. A host call which expresses human OCNCI, OCNC2 and/or betalb is useful in a mammalian cell-based assay for the profiling and screening of putative modulators of a human olfactory cyclic nucleotide gated (CNG) channel. The method is used to identify a compound as one which particularly modulates CNG activity based on a detectable change in fluorescence. The test cell expresses each of the human OCNCI, human OCNC2 and human betalb subunits. A fluorescence plate reader or a voltage imaging plate are used to monitor changes in fluorescence. The compounds that activate olfactory CNG channel enhance smell and can be used to make foods more palatable for individuals with attenuated olfactory function. The present acquence represents the amino acid sequence of human betalb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 LFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLRLKSVLYLPGDFVCKKGE1GKEMY11KHGEVQVLGGPDGTKVLVTLKAGSVFGE1SLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 KRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDM
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 AAGGGRRRTANVVAHGFANLLTLDKKTLQEILVHYPDSERILMKKARVLLKOKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AVGGGRRRTANVVAHGFTNLFILDKKDLNBILVHYPESOKLLRKKARRMLRSNNK
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                             35; indels
                                                                                                                                                                                                                                                                                                                                                                                               21.4%; Score 906; DB 6; 72.8%; Pred. No. 1.6e-68; ive 29; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 72.8
Matches 171, Conservative
                                                                                                                                                                                                                                                                                                                                                          Sequence 237 AA;
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completed: December 21, 2005, 19:54:04 Job time : 190 secs Search

Novel isolated nucleotide sequences encoding human OCNCI, OCNC2, beta 1b olfactory cyclic nucleotide gated (CNG) channel subunits, useful for identifying the CNG channel activators useful for enhancing smell.

Disclosure; Page 86; 97pp; English

Xu H, Staszewski L, Moyer B, Pronin A, Adler JE; Callamaras N;

WPI; 2003-229406/22.

Zoller MT, Servant G,

N-PSDB; ABZ80565.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

December 21, 2005, 19:47:49; Search time 43 Seconds (without alignments) 1810.218 Million cell updates/sec Run on:

US-09-855-828-1 4234 1 MFKSLTKVNKVKPIGENNEN......PSAEGGEEVLTIEVKEKAKQ 809 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

S	Description	cGMP-gated cation	hypothetical prote	cyclic nucleotide-	cAMP-gated channel	alpha subunit of c	cyclic nucleotide-		cGMP-gated cation	cGMP-gated ion cha	cyclic nucleotide-	cyclic nucleotide-	rod cyclic nucleot	cGMP-gated ion cha	cyclic nucleotide-	alpha subunit of r	hypothetical prote	DmCNGC protein - f	olfactory cyclic n		hypothetical prote	cyclic nucleotide-	О	hypothetical prote	U		potassium channel	potassium channel	potassium channel	probable potassium
SUMMARIES	a	532538	T19627	S74179	S11521	150630	835691	B42161	A42161	A44842	JH0560	S11517	JC6509	S07103	A55251	150680	S28292	S52072	159327	T20936	T20935	I78559	178560	T33125	T21969	T52046	153197	148912	T12177	T07052
	08	. 2	~	~	7	7	7	7	~	-	Н	~	7	-	~	N	N	~	7	7	~	~	~	~	~1					
	Length	906	800	695	663	735	732	688	069	989	682	664	691	9	706	645	772	665	575	673	611	261	261	644	767	828	962	989	807	845
d	Query Match	46.1	25.9	19.7	19.6	19.4	19.4	19.4	19.3	19.	19.	19.	18.9	18.8	18.8	18.2	18.2	17.0	15.1	13.1	12.5				8.7		8.2			7.6
	Score	1952	1095	834.5	829	821.5	820	819.5	818.5	818	807.5	804	801.5	797	794	171	770	718	640	555	530	484	476		366.5	マ	349	336	31.	23.
	Result No.		7	е	4	2	y	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22			25	26	27	28	29

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potassium channel	. potassium channel	probable potassium	potassium channel	cyclic nucleotide-	cyclic nucleotide	potassium channel-	probable potassium	probable calmoduli	hypothetical prote						
555349	868699	138465	T07651	T04461	T03939	S23606	S62694	T42394	A40853	T51354	T51432	F85381	T05360	T04424	G84902
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688	787 2	1159 2	883	662	887	838	857	934	1174	716	106	880	916	702	718
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7.6		7.5	7.4	7.4	7.3	7.1	7.1	7.0	6.9	6.8	6.7	6.7	6.7	9.9	9.9

ALIGNMENTS

RESULT 1

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ASSULT: 3
Sy4179
Sy4179
Sy4179
Sy4179
Sy4179
Sy616 nucleotide-gated channel protein - human
C;Species: Homo sapiens (man)
C;Accession: Sy4179
R;Yu, W.P.; Grunwald, M.E.; Yau, K.W.
FEBS Lett. 333, 211-215, 1996
A;Title: Molecular cloning, functional expression and chromosomal localization of a human A;Reference number: Sy4179
A;Accession: Sy4179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Map position: 2
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleoride of
C;Keywords: ion channel; ion transport; membrane protein
F;482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology ('AP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ž
        AKPTAVPPVKESDDKPTEHYYRLLWFKVK-KMPLTEYLKR---IKLPNSIDSYTDRLYLL 220
                                                                                                                                                                                                                     GDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFFFNHH 340
                                                                                                                                                                                                                                                                                                                           | : ::|| : |:|| | GQVKIYKDTQRHYLMTRTFKLDILSILPTDLMYFFFGKMPIWRINRVLKINSFWLLFDM 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,5
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                                                                                                                                                                                                                                                                                                                                                                                                                            464 RNREEFORKMDLALGECKKLGLKMETTNRVRDWFIYTWQQQKTLDEKKLIEKLPLKLUTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             703 MNENKGVQELKKVIEEETEKSRRQSIYYPWSTLQRDDDDEEEWNDEEDLSDVGEDFDLDP
                                                                                                                                                                                    WILLUTLAYNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLOFVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGNEYLRCYYWAVRTL1T1GGLPEPQTLFE1VFQLLNFFSGVFVFSSL1GQMRDV1GAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 QGNAYIRCFYFTAAVATSTGNNPAPTNVIEYIYMTCSWMMGVFVFALLLGGIRDIVSNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANQNYFRACMDDTIAYMNNYSI PKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVLGGPDGTKVLVTLKAGSVFGE1SLLAAGGGNRRTANVVAHGFANLLTLDKKT1,QE11,V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPDSERILMKKARVLLKOKAKTAEATPPRKDLALL----PPPKEETPKLFKTLLGGT
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                                                                                                                                                                                                                                                                                                                                                                                              LESIMDKAYIYRVIRTTGYLLFILHINACVYYWASNYEGIG-----
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19.7%; Score 834.5; DB 2;
Best Local Similarity 29.7%; Pred. No. 4.3e-44;
Matches 223; Conservative 149; Mismatches 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KQKENEDKGKENEDKDKGREPEEKPLDRP
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: ONA
A;Esperimental source: Clone C31H5
A;Experimental source: Clone C31H5
B;Cottage, A.
Bublitted to the EMBL Data Library, November 1996
A;Reference number: Z19479
A;Accession: T21863
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Cross-references: UNIPARC:UPI0000083D03; EMBL:Z81532; PIDN:CAB04328.1; GSPDB:GN00019; Experimental source: clone F36F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CESP:F36F2.5
A;Map position: 1
A;Introns: 27/3; 51/2; 142/2; 191/3; 287/3; 333/3; 355/2; 405/1; 433/2; 484/1; 508/1;
                                                                                                                                                                                                                                                                                                                                                                      680
  GSTHWVYDGVGNSYIRCYYFAVKTLITIGGLPDPKTLFEIVFQLLNYFTGVFAFSVMIGQ 536
                                                   MRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLK 500
                                                                                                                                                         TLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKE 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PV-TSEEPHTNIODKLSKKNSSGDLTTNP----DPONAAEPTGTVPEOKEMDPGKEGPN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYPPTRPPEVVIQI------DEVESPILGLIDETDDHELDG-----RLDPASSFDA 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQHTHPKEAATDPPAPRTPPEPPGSPPSSPPPASLGRPEGEEEGPA-EPEEHSVR---- 882
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19627; T21863
R;Kershaw, J
R;Kershaw, J
Submitted to the EMBL Data Library, April 1997
A;Reference number: 219153
                                                                                      MYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGGGGNRRTANVVAHGFANLLTLD
                                                                                                                                                                                                                                                                                                                                                                 KKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLFPPKEETPKLFKTLL
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25.9%; Score 1095; DB 2; Length B
Best Local Similarity 31.9%; Pred. No. 3.4e-60;
Matches 258; Conservative 153; Mismatches 301; Indels
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-800 <WIZ>
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                                                                                                                                                                                                                    ADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVAS 306
                                                                                                                                                                                                                                                                         IIPPDICYLFFGFN-PMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILH 365
                                                                                                                                                                                                                                                                                                                                 INACVYYWASNYEGIGTTRWVYDG------EGNEYLRCYYWAVRTLITIGGLPEPQTL 417
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                                                                                                                                    88 VHHQDQGPDSFPDRFRGAELKEVSSQESNAQANVGSQEPADRG-----RSAW-----PL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKTAEATPPRKULALLFPPKEETPKLFKTLLGGTGKASLARLL-----KLKREQAAQ 701
                                                                              87
                        -----RTHLEVKTSDRDLNRAENGLSRAHSSSEETS-- 43
                                                                                                                                                                                                                                                                                         NEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTPVTSEEPHTNIQDKLSKKNSSGDLTTNP
                                                      DPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPAAPVINEYADAQLHNLVKRMRQRTALY
                                                                                                           147 KKKLVEGDLSSP-----EASPQTAKPTAVPPVKESDDKPTEHYYRLLWFKVKMPL
                                                                                                                                                              ------TBYLKRIKLPNSI-DSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQT
                                                                             ---SVLQP-GIAMETRGLADSGQGSFTGQ-----GIARLSRLIFLLRRWAARH
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Camp-gated channel protein - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S1521
R;Ludwig, J.; Margalit, T.; Eismann, E.; Lancet, D.; Kaupp, U.B.
R;Ludwig, J.; Margalit, T.; Eismann, E.; Lancet, D.; Kaupp, U.B.
R;Eless Lett. 270, 24-29, 1990
A;Title: Primary structure of CAMP-gated channel from bovine olfactory epithelium.
A;Reference number: S1521; MUID:91032022; PMID:1699793
A;Accession: S1521
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-663 <LUD>
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319 259 569 610 741 20; 683 107 160 103 337 NHHLESIMDKAYIYRVIRTTGYLLFILHINACVYYWASNYEGIGTTRWVY----DGE--- 390 570 QVLGGPDGTKVLVTLKAGSVFGEISLLAAGG---GNRRTANVVAHGFANLLTLDKKTLOE 626 ---AEYTGAQOKLKORITVLETKMKONNEDDSLSDGMN 654 684 GKASLARLLKLKREQAAQKKENSEGGEEEGKENEDKQKEN--EDKQKENEDKGKENEDKD 161 SPQTAKPTAVPPVKESDDKPTEHYYRLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLL -----VLDPAGD-WYYR 320 LSREYIYCLYWSTLTLTTIGETPPPVKDEFYLFV!FDFLIGVL!FATIVGNVGSMISNMN LAIDVNPSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEV 50 EKSLKTKSTPVTSEEPHTNIQDKLSKKNSSGDLTTNPDPQNAA--EPTGTVPEQKEMDPG 3 EKANGVKSSPANNHNHAPPAIKASGKD---DHRASSRPOSAAADDTSSELOQLAEMDAP 108 KEGPNSPQNKPPAAPVINEYA-----DAQLHNLVKRMRQRTALYKKKLVEGDLSSPEA -----GPEL WLLLVTL--AYNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIOPRLOFV -GNEYLRCYYWAVRTLITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGOMRDVIGAAT ANONY FRACMDDTIAYMNNYS I PKLVQKRVRTWY BYTWDSQRMLDESDLLKTLPTTVQLA 627 ILVHYPDSERILMKKARVLLKQKAKTAE---ATPPRKDLALLFPPKEETPKLFKTLLGGT Indels 60 QQRRGGFRIARLVGVLREWAYRNFREEEPRPDSFLERFR----104 HTVTTQQGDGKGDKDGEGKGTKKKFELF------11 Similarity 29.9%; Pred. No. 8.7e-44; 218; Conservative 132; Mismatches 283; 750 663 611 LYTRFARLL---742 KGREPEEKP SPEPPAEKP Local Similarity 221 260 450 380 210 559 555 338 391 Best Loca Matches g 유 g ò g ò 셤 ò g ò 9 ò g ò 요 ò 윱 ò ò 8 ò ઠે 셤 셤 ઠે

A;Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels A;Reference number: 150630; MUID:93264082; PMID:7684234 R.S.; Kaupp, alpha subunit of cone photoreceptor CNG-channel - chicken C;Species: Gallus gallus (chicken) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 C;Accession: ISO630 Molday, .. Σ R;Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, Neuron 10, 865-877, 1993

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-735 = BON>
A;Residues: 1-735 = BON>
A;Cross-references: UNIPROT:Q90805; UNIPARC:UPI0000127ClA; EMBL:X89598; NID:g908850; PID
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
F;524-648/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP> A;Cross-references: UNIPROT:Q03041; UNIPARC:UP10000127C1D; GB:X55010; NID:g287743; PIDN: C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-F;454-578/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

A; Accession:

Match Query

Score 829; 19.68;

663; Length DB 2;

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Egated cation channel, rod photoreceptor - mouse CiSpecies: Mus musculus (house mouse)
CiDate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul 1999
CiAccession: B42161
A;Pittle: Primary structure and chromosomal localization of human and mouse: rod photoreceptary and excession: B42161
A;Reference number: A42161; MUID:92210603; PMID:1372902
A;Rocession: B42161
A;Residues: 1-688 APIT>
A;Residues: 1-688 APIT>
A;Rosidues: 1-688 APIT>
A;Cross-references: UNIPARC:UPI000017789A; GB:M84742
A;Cross-references: UNIPARC:UPI000017789A; GB:M84742
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide binding
C;Reywords: CGMP binding
C;Reywords: CGMP binding
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                                                                                   -----DAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPVKESDDKPT
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                                                                                                                                                                                                                                                                                                                     LVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTK
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                                                                                                                                            -----GPELQTVTTQQGDGKGDKDGDGKGT
                                                                                                                                                                                                    EHYYRLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTL--AYNWNCWFIPLR
                                                                                                                                                                                                                                                          ------VLDPAGD-WYYRWLFVIAMPVLYNW-CLLV AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 YILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 IPKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLLFILHINACVYYWASNYEGIGTTRWVY - - - - DGE - - - - GNEYLRCYYWAVRTLITIGG
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19.4%; Score 819.5; DB 2;
Best Local Similarity 30.8%; Pred. No. 3.6e-43;
Matches 193; Conservative 134; Mismatches 238;
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A;Cross-references: UNIPARC:UPI0000047179; EMBL:X59668; NID:g433959; PIDN:CAA42201.1; PI
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F;522-646/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
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cyclic nucleotide-gated channel protein - rabbit

cyclic nucleotide-gated channel protein - rabbit

cyclic nucleotide-gated channel protein - rabbit)

C;Species Oryclolagus cuniculus (domestic rabbit)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999

C;Accession: S35691

K;Biel, M.; Altenhofen, W.; Hullin, R.; Ludwig, J.; Freichel, M.; Flockerzi, V.; Dascal, FBBS Lett. 39, 134-138, 1993

A;Title: Primary structure and functional expression of a cyclic nucleotide-gated channel A;Reference number: S35691; MUID:93359035; PMID:7689061
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                                                                                                                                                                            SSNMYYNWLTIIAAPVEYNW-CMLI-CRACFDELQIDHIKLWLFLDYCSDIIYVFDM-FV 262
                                                                                                                                                                                                                                                          QPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFGFN-PMFRANRMLK 330
                                                                                                                                                                                                                                                                                           331 YTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACVYYWASNYEGIGTTRWVYDGE 390
                                                                                                                                                                                                                                                                                                                                                                                                         323 IARLFEFFDRTETRINYPNMFRIGNLVLYILIIHWNACIYFAISKVIGFGTDSWVYPNV 382
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                                                                                                                                         214 TDRLYLLWLLLVT--LAYNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMY
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19.4%; Score 820; DB 2; Length 732;
Best Local Similarity 28.8%; Pred. No. 3.6e-43;
Matches 222; Conservative 132; Mismatches 306; Indels 112;
                                                                                   49;
                             735;
                             Length
                                                                                   Indels
                       Query Match
19.4%; Score 821.5; DB 2;
Best Local Similarity 34.7%; Pred. No. 3e-43;
Matches 189; Conservative 110; Mismatches 196;
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Db 72 R-KGGPSQREQYLPGAIAIFNVNNSSNKDQEPEEKKKKKEKKSKSDDKNE 121 Qy 114 PONKPPAAPVINEYADAOLHNLVKRMRORTALYKKLVEGDLSSPEASPOTAKPTAVPPV 173 122 NKWDPE		Oy 523 DERGOTOGNIA TOPALLERS VILLED FOR KNEET CHANTING EVOLUCIONISTIC SELECTION OF STATE AND STATE STA	RESULT 9 A44442 cGMP-gated ion channel protein - human N;Alternate names: rod photoreceptor cGMP-gated channel C;Species: Home sapiens (man) C;Accession: A44842 R;Dhallan, R.S.; Macke, J. P.; Eddy, R.L.; Shows, T.B.; Reed, R.R.; Yau, K.W.; Nachans, J. A;Ttle: Human rod photoreceptor CGMP-gated channel: amino acid sequence, gene structur: A;Reference number: A44842; MUID:92356211; PMID:1379636 A;Residues: 1-686 cDHXA A;Residues: 1-686 cDHXA A;Residues: Lefe cDHXA A;Residues: Loss contracted from NCBI backbone (NCBIN:110250, NCBIP:110251) A;Note: intron positions were determined from genomic sequence C;Genetics: A;Gene: GDB:CNCG; CGC A;Cross-references: GDB:127557; OMIM:123825 A;Mat position: 4p14-4q13 A;Introns: 36(2:75/2:75/2:75) A;Introns: 36(2:75/2:75/2:75/2:75/2:75/2:75/2:75/2:75/
106 PGKEGPNSPQNKPPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGD 154 106 PGKEGPNSPQNKPPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGD 154 106 PG	273 PRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFGFN-PMFRANRMLKY 331 215 TRTGYLEGGLLVKDRMKLIEKYKANLOFKLDVLSVIPTDLLYIKFGWNYPEIRLNRLIRI 274 332 TSFFFFNHHLESIMDKAYIYRVIRTTGYLLFILHINACVYYWASNYEGIGTTRWYY 387 275 SRMFEFFORTETRTNYPNIFRISNLVMYIVIIHWNACVYYSISKAIGFGNDTWYPDVN 334 386 DGEGNEYLRCYYWAVRTLITIGGLPEPOTLFFIVFQLLNFFSGVFVESSLIGGMRD 443 387 PFFFRANKVYSLYWSTLITIGGLPEPOTLFFIVFQLLNFFSGVFVESSLIGGMRD 443 444 VIGAATANQNYFRACMDDTIAYMNYSIPKLVQKRYRTWYWYFTWDSQRMLDESDLLKTLP 503 1	504 TTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYI 563 :: : : : : : :	A42161 cGMP-gated cation channel, rod photoreceptor - human C;Species: Homo sapiens (man) C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004 C;Accession: A42161 R;Pittler, S.J.; Lee, A.K.; Altherr, M.R.; Howard, T.A.; Seldin, M.F.; Hurwitz, R.L.; Wa A;Titler, Primary structure and chromosomal localization of human and mouse rod photorece A;Reference number: A42161; MUDD:92210603; PMID:1372902 A;Accession: A42161 A;Residues: 1-690 *PIT> A;Residues: 1-690 *PIT> A;Residues: 1-690 *PIT> A;Residues: 1-690 *PIT> A;Cosserences: UNIPROT:P29973; UNIPARC:UPI0000163B2A; GB:M84741; NID:g180461; PIDN: C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide- C;Keywords: CGMP binding; transmembrane protein C;Keywords: CGMP binding; transmembrane C;Keywords: CGMP binding; trans

Tue Dec

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A, Experimental source: olfactory epithelium
C, Comment: This cyclic nucleotide-gated channel is activated equally well by both cAMP in C, Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide (C, Superfamily: cyclic nucleotide) and comment in the cyclic nucleotide (C, Keywords: CAMP binding; cGMP binding; lon channel; and transport; olfaction; transmembrane #status predicted (TS1)
F;173-193/Domain: transmembrane #status predicted (TS2)
F;217-236/Domain: transmembrane #status predicted (TS3)
F;272-277/Domain: transmembrane #status predicted (TS5)
F;373-370/Domain: transmembrane #status predicted (TS5)
F;373-370/Domain: transmembrane #status predicted (TS5)
F;373-377-277/Domain: transmembrane #status predicted (TS5)
F;373-370/Domain: transmembrane #status predicted (TS5)
F;373-370/Domain: compression for the complex for
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                                                                                                  LTKVNKVKPIGENNENEQSSRRNEEGSHPS-----KSL
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                                                                Gaps
                    Query Match
19.3%; Score 818; DB 1; Length 686;
Best Local Similarity 29.9%; Pred. No. 4.4e-43;
Matches 226; Conservative 129; Mismatches 266; Indels 136;
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148

PAAPVINEYAD-----SPQTHNLVKRMRQRTALYKKKLVEGDLSSPEA----SPQTAKPT

77;

Length 682, Indels

DB 1;

19.1%; Score 807.5; DB 1; llarity 29.0%; Pred. No. 2e-42; Conservative 137; Mismatches 256;

Similarity

192;

119 55 169 111

AVPPVKESDDKPTEHYYRLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLA

--YNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVD

229

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RESULT 11
S11517
cyclic nucleotide-activated channel protein - rat
cyclics. Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-C;Accession: S11517
R;Dhallan, R.S.; Yau, K.W.; Schrader, K.A.; Reed, R.R.
                                                                                                                        681
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                                                                                                                                                              S.A.; Chesa
                                                                                                                                                                                                                              cyclic nucleotide-gated
                                                                                                                                                          S.; Axel, R.; Siegelbaum,
                                     Species: Ictalurus punctatus (channel catfish)
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
cyclic nucleotide-gated channel - channel catfish
CySpecies: Ictalurus punctatus (channel catfish)
CyDate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Ju
CyAccession: JH0560
R;Goulding, E.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Sieg
Neuron 8, 45-58, 1992
A;Title: Molecular cloning and single-channel properties of the cycli
A;Reference number: JH0560; MUID:92110008; PMID:1370374
A;Accession: JH0560
A;Status: nucleic acid sequence not shown
A;Mesidues: 1-682 cGGU>
A;Residues: 1-682 cGGU>
A;Residues: 1-682 cGGU>
A;Cross-references: UNIPROT:P55934; UNIPARC:UPI0000127C25; GB:M83111
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Jul 2004

619 619 346 20% 265 402 325 462 385 522 504 564 683 505 LLTAGGCFGEISILNIQGSKMGNRRTANIRSIGYSDLFCLSKDDLMEAVAEYPDAQKVLE SLYNW -- IMLVARACFDQLQDENFFLWVGLDYLCDV1Y1LDTC - IRLRTGYLEQXILLVKI) SNELRKHYRTSTKFQLDVASI1PFDICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMD KAYIYRVIRTTGYLLFILHINACVYYWASNYEGIGTTRWVYDGEGNE----YLRCYYWAV YPNAFRICNLILYILVIHWNACIYYAISKALGLSSDTWVYSGONKTLSFCYVYCFYWST 620 ORRLKORITALEROLCHTGLGLLSDNEAEGEHAGVPTHTHADIHAOPETHTRTSAETNSE RTLITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDT IAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKV DLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLV TLKAGSVFGEISLLAAGG----GNRRTANVVAHGFANLLTLDKKTLQEILVHYPDSERILM KKARVLLKQKAKTAEATP-------PRKDLALLFPPKEETPKLFKTLLG---GT GKASLARLLKLKREQA----AQKKENSEGGEEEG---KENEDKQKENEDKQKENEDKGKE NE 738 287 684 737 149 347 403 463 386 583 640 565

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cGMP-gated ion channel protein
                                                                                                                                                                                                Similarity
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Nature 347, 184-187, 1990

A,Title: Primary structure and functional expression of a cyclic nucleotide-activated change termine number: $11517; MUID:90370115; PMID:1697649

A,Reference number: $11517; MUID:90370115; PMID:1697649

A,Residue: $11517

A,Residue: $1.64 cDHA>

A,Residue: 1.64 cDHA>

A,Residue: 1.64 cDHA>

A,COSS-references: UNIPROT:000195; UNIPARC:UPI0000000CF3; GB:X55519; NID:956791; PIDN:CC; Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-C:Keywords: transmembrane protein
C; Keywords: transmembrane protein
F; 456-580/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology cCAP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQVLGGPDGTKVLVTLKAGSVFGEISLLAAGG---GNRRTANVVAHGFANLLTLDKKTLQ 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EILVHYPDSERILMKKARVLLKOKAKTAE---ATPPRKDLALLFPPKEETPKLFKTLLGG 682
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EAVTEYEDAKKVLEERGREILMKEGLLDENEVAASMEVDV-----QEKLEQLETNM--D 611
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C;Species: Canis lupus familiaris (dog)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 YLAREYIYCLYWSTLTLTTIGETPPPVKDEBYLFVIFDFLIGVLIFATIVGNVGSMISNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 EKSLKTKSTPVTSEEPHTNIQDKLSKKNSSGDLTTNPDPQNAAEPTGTVPEQK---EMDP
                                                                                                                                                                                                                                   107 GKEGPNSPQNKPPAAPVINEYADAQLH------NLVKRMRQRTALYKKKLVEGDLSSPE
                                                                                                                                                                                                                                                                                                                               ASPQTAKPTAVPPVKESDDKPTEHYYRLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYL
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                                                                                                                                                                                    286; Indels 108;
                                                                                                                                                     Match 19.0%; Score 804; DB 2; Length 664; Local Similarity 29.6%; Pred. No. 3.1e-42; les 219; Conservative 126; Mismatches 286; Indels 10
                                                                                                                                                                                                                                                                                                PRRGRGGFORIVRLVGVIRDWANKNFREEEPRPDSFLERFR-----
                                                                                                                                                                                                                                                                                                                                                         LQTVTTHQGDDKGGKDGEGKGTKKKFELF--
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SDG-----INTPEPTAA 663
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C;Accession: JC6509
R;Veske, A.; Nilseon, S.E.G.; Gal, A.
Acrees and S.E.G.; Gal, A.
Acrees and S.E.G.; Gal, A.
Acrees and S.E.G.; Gal, A.
A;Reference number: JC6509; MUD: 98087425; PMID: 9427553
A;Recession: JC6509
A;Status: preliminary
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-691 «VES>
A;Cross-references: UNIPROT: Q28279; UNIPARC: UPI0000127C19; EMBL: X99914; NID: 91488571; PII
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-1
F;778-602/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology «CAP»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FN-PMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACVYYWASNY 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 IGFGNDTWVYPDVNDPEFGRLARKYVYSLYWSTLTLTTTIGETPPPVRDSEYVFVVVDFLI 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 EKETRRMENGARSS-----FSDDDGDDDSASMFEES---ENETPHA--RDSCRNNSORR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 DLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPAAPVINEYADAQLHNLVKRMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 QRTALYKKKLVEGDLSSPEASPQTAKPTAVPPVKESDDKPTEHYYRLLWFKVKKMPLTEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 KKKK--EKKSKSGDKNENKKDSEKKKKKE----KEKEKKNKEEK----GKDKK---EEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 LKRIKLPNSIDSYTDRLYLLWLLLVTL--AYNWNCWFIPLRLVFPYQTADNIHYWLIADI
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Indels 112;
                                                                                                                                                                                                                                                                                                                                                        Length 691;
                                                                                                                                                                                                                                                                                                                                                     18.9%; Score 801.5; DB 2;
ilarity 29.2%; Pred. No. 4.7e-42;
Conservative 136; Mismatches 286;
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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S07103
Nature 342, 762-766, 1989
N;Kaupp, U.B.; Nidome, T.; Tanabe, T.; Terada, S.; Boenigk, W.; Stuehmer, W.; Cook, N.J.
Nature 342, 762-766, 1989
A;Hitle: Primary structure and functional expression from complementary DNA of the rod pA;Recession: S07103
A;Recession: S07103
A;Accession: S07103
A;Accession: NOT Compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-690 cKAU
A;Residues: 1-690 cKAU
A;Residues: 1-690 cKAU
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-C;Reywords: CGMP binding; eye; ion channel; ion transport; retina; transmembrane protein F;477-601/Domain: CAMP receptor protein cyclic nucleotide-C;Reywords: CGMP binding; eye; ion channel; ion transport; retina; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 YADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPVKESDDKPTEHYYR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 NNSSNKEQEPKEKKKKKK--EKKSKPDDKNENKKDPEKKKKKE----KDKDKKKKEE--- 140
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                                                                                                                                                                                                                                                                                                                                            VNKVKPIGENNENEQSSRRNEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTPVTSEEPHT
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                           Query Match
18.8%; Score 797; DB 1; Length 690;
Best Local Similarity 29.3%; Pred. No. 9e-42;
Matches 212; Conservative 129; Mismatches 282; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                       60 ---RDSFRSNTHGSGQ-----
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VEK 662
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cyclic nucleotide-gated Ca++ channel protein CNG-3 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Sacesion: A55251; 84936
R;Blel, M.; Zong, X.; Distler, M.; Bosse, E.; Kluqbauer, N.; Murakami, M.; Flurkwirzi, V. Proc. Natl. Acad. Sci. U.S.A. 9, 1305-13509, 1994
A;Title: Another member of the cyclic nucleotide-gated channel tamily, expirasional A5251; MUD:94224768; PMID:8170936
A;Tatus: nucleic acid sequence not shown
A;Scatus: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Title: Cloning and functional expression of a cyclic-nucleotide-gated channel from murative 368, 859-863, 1994
A;Title: Cloning and functional expression of a cyclic-nucleotide-gated channel from murative 368, 859-863, 1994
A;Reference number: 843976; MUD:94211295; PMID:7512693
A;Status: preliminary; nucleic acid sequence not shown
A;Residues: 1-706 ANDA
A;Re
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18.8%; Score 794; DB 2; Length 70
Best Local Similarity 29.7%; Pred. No. 1.4e-41;
Matches 204; Conservative 141; Mismatches 263; Indels
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Job time : 47 secs
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A; Residues: 1-645 <BON>
A; Cross-references: UNIPROT: Q90980; UNIPARC: UPI0000127C21; EMBL: X89599; NID: g908852; PIC
C; Superfamily: cyclic nuclectide-gated channel; cAMP receptor protein cyclic nucleotide-
F; 431-555/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
                                                                                                                                                                                                                                                                                                       alpha subunit of rod photoreceptor CNG-channel - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150680
R;Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.E Neuron 10, 865-877, 1993
A;Title: Rod and cone photoreceptor cells express distinct genes for CGMP-gated channels A;Reference number: 150630; MUID:93264082; PMID:7684234
A;Reference number: ISO630; MUID:93264082; PMID:7684234
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532 DLMEALTEYPDAKAMLEEKGKQILMKDGLLDIEVANLGSD-----PKDLEEKV--AYME 583
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                         VLGGPDGTKVLVTLKAGSVFGEISLLAAGG---GNRRTANVVAHGFANLLTLDKKTLQEI 627
                                                                                  LVHYPDSERILMKKAR-VLLKQK---AKTAEATPPRKDLALLFPPKEETPKLFKTLLGGT 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 LYLLWLLLVTL--AYNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPR
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18.2%; Score 771; DB 2; Length 645;
Best Local Similarity 34.3%; Pred. No. 3.4e-40;
Matches 173; Conservative 104; Mismatches 196; Indels
                                                                                                                                                                  GKASLARLL-----KLKREQAAQKKEN 705
                                                                                                                                                                                         GTG---KASLARLLKLKREQAAQKK 703
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Search completed: December 21, 2005, 19:58:54

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Sequence 19, Appl
Sequence 1037, Ap
Sequence 11549, A
Sequence 1, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 46624, Appl
Sequence 6615, Appl
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6615, Ap
2, Appli
10771, Appl
10774, Ap
6036, Ap
7263, Ap
10, Appli
4, Appli
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/ cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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// cgn2_6/ptodata/1/iaa/RECOMB.pep:*
// cgn2_6/ptodata/1/iaa/RECOMB.pep:*
// cgn2_6/ptodata/1/iaa/RECOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-538-092-1351
US-09-538-092-1351
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US-09-949-016-10215
US-09-97-267-1
US-09-977-267-1
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US-09-949-016-6036
US-09-086-436-33
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RESULT 1
US-09-949-016-6945
; Sequence 6945. Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: PSECSE for Windows Version 4.0
; SEQ ID NO 6945
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Pred, No. 4e-272;
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                                                                 US-09-694-777A-3
US-10-422-075-9
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US-10-162-012-12
US-09-614-480-2
US-10-162-012-5
US-10-162-012-5
US-10-422-075-2
US-09-3813C-22
US-09-694-777A-4
US-09-956-242-13
US-09-226-012-2
-09-694-777A-22
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Best Local Similarity 99.0%;
Matches 609; Conservative
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SSLIGOMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLD 494

SNYEGIGTTRWVYDGEGNEYLRCYYWAVRTLITIGGLPEPQTLFEIVFOLLNFFSGVFVF 434

375 181 435

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301 ----QFPQSIDPLTNLMYVLWLFFVVMAWNWNCWLIPVRWAFPYQTPDNIHHWLLMDYLK 356
                                   301 PQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 --SPQNKP-----PAAP------VINEYADAQLHNLVKRMRQRTALY 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 IGENNENEQSSRRNEEGSHPSNQSQQTTAQE--ENKGE---EKSLKTKSTPVTSEEPHTN
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                                                                                                                                                                                                                            APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same:
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/518,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARES CURRENTER CURRENTER CONS: 1387
SEQ ID NO 1315
LENGTH: 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 IQDK-----LSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPN----
                                                                                    474 LVOKRVRIWYEYIWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 46.0%; Score 1949; DB 2; Length 909; Best Local Similarity 46.2%; Pred. No. 9e-164; Matches 403; Conservative 122; Mismatches 238; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LUCATION: (U)...(V)

7  OTHER IN-PORMATION: Polypeptide Accession Number Q14028
US-09-588-092-13115
                                                                                                                                                                              ; Sequence 1315, Application US/09538092; Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                 US-09-538-092-1315
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Fatent No. 6812339
GENERAL INFORMATION: Craig et al.
FAPPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT FILING DATE: 2000-04-14
PRIOR PPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-0-08
PRIOR FILING DATE: 2000-0-0-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                               LFKTLLGGTGKASLARLLKLKREQAAQKKENSEGGEEGGKENEDKQKENEDKQKENEDKG 734
                                                                                                                                                                                                                                            KENEDKDKGREPEEKPLDRPECTASPIAVEEEPHSVRRTVLPRGTSRQSLIISMAPSAEG 794
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99.8%; Pred. No. 9.2e-187;
tive 0; Mismatches 1;
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Best Local Similarity 99.8
Matches 412; Conservative
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US-09-949-016-11669
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RESULT 5
US-09-538-092-1351
; Sequence 1351, Application US/09538092
; Patent No. 675314
; REMEMAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Giot, Loic
; TILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT PELLONG DATE: 2000-03-29
; PRIOR PILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NOS: 1387
; JEDNATH: 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 DPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPAAPVINEYADAQLHNLVKRMRQRTALY 146
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                                                                                                                                         GLPEPQTLFEIVFQLLNFFSGVFVFSSLIGOMRDVIGAATANONYFRACMDDT1AYMNNY 469
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                                                                                                                                                                                                                                                                      492 AGLIVELVLKIRPTVFSPGDYICKKGDIGKEMYIINEGKLAVV-ADDGVTOFVVLSDGSY
                                                                                                                                                                                                                                                                                                                                                                                                KFOLDVASIIPFDICYLFFGFN-PMFRANRMLKYTSFFEFNHHLESIMDKAY1YRV1RTT
                                                                                                                       GYLLFILHINACVYYWASNYEGIGTTRWVYDG------EGNEYLRCYYWAVRTLITIG
                                                                                                                                                                                                                                                   SIPKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCD
                                                                                                                                                                                                                                                                                                                   530 TQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSV
                                                                                                                                                                                                                                                                                                                                                                                 590 FGEISLLAAGG---GNRRTANVVAHGFANLLTLDKKTLOEILVHYPDSERILMKKAR-VL
RLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTST
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
COTHER INPOMENTION: Polypeptide Accession Number Q16281
US-09-28-092-1351
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Matches
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Sequence 10215, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOG.1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SQO ID NO 10215

LENGTH: 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 MRORTALYKKKLVEGDLSSP-----EASPQTAKPTAVPPVKESDDKPTEHYYRLLW 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 FKVKKMPL-----TEYLKRIKLPNSI-DSYTDRLYLLWLLLVTLAYNWNCWFIPL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           882
MYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGGGNRRTANVVAHGFANLLTLD 620
                                                                                                                                                                            KKTLQEILVHYPDSERILMKKARVLLKQKAKTARATPPRKDLALLFPPKEFTPKLFKTLL 680
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                                                                                                                                                                                                                                                           -----EEEPHSVRRTVLP 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 ENEQSSRRNEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTPVTSEEPHTNIQDKLSKKNS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  829 DOHTHPKEAATDPPAPKTPPEPP-GSPPSSPPPASLGSCEGEEGGPAEPEEKSVR----
                                                  TLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKE
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                                                                                                                                                                                                                                                                                                       729 ENEDKGKE-NEDKDKGREPEEKPLDRPECTASPIAV----
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US-09-949-016-10215
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Sequence 19, Application US/09275252A

Sequence 19, Application US/09275252A

Sequence 19, Application US/09275252A

GENERAL INFORMATION:

APPLICANT: MacKinnon, Roderick

APPLICANT: The Rockefeller University

TITLE OF INVENTION: Assays for Screening Compounds Which Interact With

TITLE OF INVENTION: Cation Channel Proteins, Mutent Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof

FILE REPERENCE: 018512-00290108

CURRENT APPLICATION NUMBER: US/09/275,252A

CURRENT FILING DATE: 1999-03-24

PRIOR PILING DATE: 1999-03-20

PRIOR APPLICATION NUMBER: US 09/054,347

PRIOR PILING DATE: 1999-04-02

PRIOR PILING DATE: 1999-04-02

PRIOR PILING DATE: 1999-03-22

PRIOR PILING DATE: 1999-03-22

PRIOR FILING DATE: 1999-03-22
                                                                                 88 VHHQDQGPDSFPDRFRGAELKEVSSQESNAQANVGSQEPADRG----RSAW-----PL 136
                                                                                                                              ------TEYLKRIKLPNSI-DSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQT 246
                                                                                                                                                   137 AKCNTNTSNNTEEEKKTKKKDAIVVDPSSNLYYRWLTAIALPVFYNWYLLICRACFDELQ 196
                                                                                                                                                                                                  ADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVAS 306
                                                                                                                                                                                                                       SEYLMLWLVLDYSADVLYYLDVL-VRARTGFLEGGLMYSDTNRLWQHYKTTTGFKLDVLS 255
                                                                                                                                                                                                                                                                         307 IIPPDICYLFFGFN-PMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILH 365
                                                                                                                                                                                                                                                                                             366 INACVYYWASNYEGIGTTRWVYDG------EGNEYLRCYYWAVRTLITIGGLPEPQTL 417
                                                                                                                                                                                                                                                                                                                                                                     316 WNACIYFAISKFIGFGTDSWVYPNISIPEHGRLSRKYIYSLYWSTLTLTTIGETPPPVKD 375
                                                                                                                                                                                                                                                                                                                                                                                                                     FEIVFQLLNFFSGVFVFSSLIGOMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVQK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                           RVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDML 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLA 597
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 703 KENSEGGEE---EGKENEDKOKENEDKOK 728
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ORGANISM: Homo
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US-09-275-252A-19
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                                                                                                                                                       54 KTKSTPVTSEEPHTNIQDKLSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNS 113
                                                                                                                                                                            114 PQNKPPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPV 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       537 VLSDGSTFGEISILNIKGSKAGNRRTANIKSIGYSDLFCLSKDDLMEALTEYPDAKTMLE 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTLITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LTKVNKVKPIGENNENEQSSRRNEEGSHPS----NOSQQTTAQEENKGEE-----KSL
                                                                                                               NCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELR
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                                                             Gaps
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Batent No. 6753314

Batent No. 6753314

Batent No. 6753314

BAPLICANT: NORMATION:

APPLICANT: Mansfield, Traci A.

APPLICANT: Mansfield, Traci A.

TILLE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR PELING DATE: 1999-04-01

PRIOR PELING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/179,965
                                                                                                                                                                                                                                                                               174 KESDDKPTEHYYRLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTL
                                                             125;
                              Length 690;
                                                             Indels
                             tch 19.3%; Score 818.5; DB 2; al Similarity 30.0%; Pred. No. 1.3e-63; 221; Conservative 128; Mismatches 262;
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                         Query Match
Best Local Similarity
Matches 221; Conserv
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US-09-275-252A-19
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ORGANISM:
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                                                                                                                                                                                                                                                                     54 KTKSTPVTSEEPHTNIQDKLSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNS 113
                                                                                                                                                                                                                                                                                               68 R-KGGPSQREQYLPCALALFNVNNSS-----NKD----QEPEEKKKKKKKKKKKSKSDDKNE 117
                                                                                                                                                                                                                                                                                                                        PONKPPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPV 173
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                                                                                                                                                                                                                                                                                                                                                                                                                            NCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELR 291
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                                                                                                                                                                                          Gaps
                                                                                                                                                                Query Match 19.3%; Score 817; DB 2; Length 686; Best Local Similarity 29.9%; Pred. No. 1.8e-63; Matches 226; Conservative 129; Mismatches 266; Indels 136;
                                                                                                             ; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P29973
US-09-538-092-1037
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PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SEQ ID NO 1037
                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                    NAME/KEY: misc_feature
                                                    LENGTH: 686
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S-09-949-016-11549 Sequence 11549, Application US/09949016

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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREDF.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREDF.
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
SOUTHARD FRIOR FLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHARD FRIOR FRIENG FARESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 11549
LENGTH: 694
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19.3%; Score 817; DB 2; Length 694;
Best Local Similarity 29.9%; Pred. No. 1.8e-63;
Matches 226; Conservative 129; Mismatches 266; Indels 136;
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US-09-949-016-11549
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; Sequence 18, Application US/09275252A
; Patent No. 6641997
                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Rattus norvegicus
                                     RESULT 10
US-09-927-267-16
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                                                                                                Sequence 1, Application US/09927267

Sequence 1, Application US/09927267

Patent No. 6933147

GENERAL INFORMATION:

APPLICANT: Creech, Christopher D.

APPLICANT: ICAGEN, Inc.

TITLE OF INVENTION: Channel

TITLE OF INVENTION: Channel

TITLE OF INVENTION: Channel

TITLE OF INVENTION: Channel

FILE REFERENCE: 018512-006510US

CURRENT APPLICATION NUMBER: US/09/927,267

CURRENT PILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 16

SSOFTWARE: Patentin Ver. 2.1

SSO ID NO 1

LENGTH: 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACVYYWASNYEGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
15.5%; Score 655; DB 2; Length 575;
Best Local Similarity 29.2%; Pred. No. 3.3e-49;
Matches 165; Conservative 121; Mismatches 241; Indels
                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: cyclic nucleotide-gated cation channel US-09-927-267-1
                                     ESMOOKLKQRLTKVEKFLKPLIDTEFSSIEGPGAESG 689
            ---ENSEG-GEEEG
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            ----KLKREQAAQKK---
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GENERAL INFORMATION:
APPLICANT: Creech, Christopher D.
APPLICANT: Creech, Timothy J.
APPLICANT: ICAgen, Inc.
TITLE OF INVENTION: CNG2B: A No. 6933147el Human Cyclic Nucleotide-Gated Ion
TITLE OF INVENTION: Channel
FILE REFERENCE: 018512-006510US
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/226,253
PRIOR APPLICATION NUMBER: US 60/226,253
PRIOR PLING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLQEILVHYPDSERILMKKAR-VLLK-----QKAKTA--EATPPRKDLALLFPPKEE 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 NTADAAFY---PDHALVKKYMKLQHVNKRLERRVIDWYQHLQINKKMTNEVAILQHLPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566 HGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGG---GNRRTANVVAHGFANLLTLDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 VRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFGFN-PMFRANRMLKYTSFFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           506 VQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 YLLWLLLVTLAYNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 YYWWLNTMVFPIMYNLIIVVCRACFPDLQHSYLVAWFVLDYTSDLLYLLD IGVRFHTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: rat cyclic nucleotide gated cation channel UCNC2
US-09-927-267-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 FNHHLESIMDKAYIYRVIRTTGYLLFILHINACVYYWASNYEGIGTTRWVYDGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
15.1%; Score 640; DB 2; Length 575
Best Local Similarity 29.1%; Pred. No. 7.1e-48;
Matches 157; Conservative 114; Mismatches 224; Indels
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Sequence 16, Application US/09927267
Patent No. 6933147
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RESULT 13
US-09-949-016-6615
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APPLICANT: MacKinnon, Roderick
APPLICANT: MacKinnon, Roderick
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Channel Proteins, and Uses Thereof
FILE REFERENCE: 018512-002901US
CURRENT APPLICATION NUMBER: US 09/045,529
PRIOR APPLICATION NUMBER: US 09/045,529
PRIOR FILING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR PLING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SSEC ID NO 18
LENGTH: 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 VYYWASNYEGIGTTRWVY----DGE----GNEYLRCYYWAVRTLITIGGLPEPQTLFEIV 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOLLNFFSGVFVFSSLIGOMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVOKRVRT 481
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US-09-270-767-46624
US-09-270-767-46624

Sequence 46624, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melànogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 46624

LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
11.4%; Score 484; DB 2; Length 261;
Best Local Similarity 37.2%; Pred. No. 1.5e-34;
Matches 97; Conservative 58; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa means any amino acid
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ORGANISM: Drosophila melanogaster
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US-09-275-252A-18
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Matches 78; Conserva
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253 WLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDI 312

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Sequence 6615, Application US/09949016

Sequence 6615, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 6615

LENTH: 1203
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                                                                                                                                                                                                                                                    62 SEEPHINIQDKLSKKN--SSGDLTINPD---PONAAEPTGTVPEOKEMDPGKE----GP
45 WLACOPCADIIYLLDVVFFKHRVMYLFEGFWVKNKTFTKNYMRKLQFKLDLLALLPLEL
                                                                                                                                313 CYLFFGFNPMF-RANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACVY
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9.8%; Score 413; DB 2;
Best Local Similarity 23.9%; Pred. No. 3.2e-27;
Matches 152; Conservative 109; Mismatches 273;
                                                                                                                                                                                                                                                                                                                                              432 FVFSSLIGOMRDVIGAATANONYFRACMDDTI 463
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FVFALLIGQIRDIISTATRNKHEYROLEDETL 256
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Patent No. 6551821
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University
APPLICANT: Kandel, Eric
TILLE REFERENCE: 0575/54806
CURRENT APPLICATION NUMBER: US/08/997,685A
CURRENT FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
FEMALE: PATENTING NOS: 60
SOFTWARE: Patentin version 3.1
               MLDESDLLKTLPTTVQLALAIDVNFS---IISKVDLFKGCDTQMIYDMLLRLKSVLYLPG 548
                                                                 WFDEESILGELSEPLREEI --- INFNCRKLVASMPLFANADPNFVTSMLTKLRFEVFQPG 619
                                                                                       DFVCKKGEIGKEMYIIKHGEVQVL-GGPDGTKVLVTLKAGSVFGEISLLAAGGGNRRTAN 607
                                                                                                    FVFSSLIGOMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVOKRVRTWYEYTWDSQR 491
                                                                                                                                   VVAHGFANLLTLDKKTLQEILVHYPDSERILMKKA 642
                                                                                                                                                  9.7%; Score 412.5;
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DATABASE ENTRY DATE: 1997-12-27
RELEVANT RESIDUES: (1)..(910)
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OTHER INFORMATION: CNB
PUBLICATION INFORMATION
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OTHER INFORMATION: S4
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INFORMATION: P
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INFORMATION: S6
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OTHER INFORMATION: S1
FEATURE:
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OTHER INFORMATION: S2
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OTHER INFORMATION: S3
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OTHER INFORMATION: SS
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ORGANISM: mouse
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APPLICANT: Kandel, Eric R.
APPLICANT: Santoro, Bina
APPLICANT: Sartsch, Dusan
APPLICANT: Siegelbauw, Steven
APPLICANT: Siegelbauw, Steven
APPLICANT: Tibbs, Gareth
APPLICANT: Tibbs, Gareth
APPLICANT: Tibbs, Gareth
TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 0575/54806-A
CURRENT APPLICATION NUMBER: US/09/086,436
CURRENT FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 67
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ed. No. 2.3e-27;
Mismatches 269;
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Patent No. 6703485
GENERAL INFORMATION:
                            Conservative 144;
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                                                                                            Query Match 9.7%; Score 412.5; DB 2; Length 910; Best Local Similarity 20.2%; Pred. No. 2.3e-27; Matches 150; Conservative 144; Mismatches 269; Indels 179; Gaps
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Job time : 51 secs
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816 HEVSTLIS-RPHPTVGESLASI 836
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SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 31 LENGTH: 910
                                         TYPE: PRT
CRGANISM: Murine
US-09-086-436-31
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                           1867569 seqs, 417829326 residues
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Sequence 1, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: Creech, Christopher D.
    APPLICANT: Jegla, Timothy J.
    APPLICANT: ICAGen, Inc.
    TITLE OF INVENTION: CNG1812-006010US
    CURRENT APPLICATION NUMBER: US/09/855,828
    CURRENT PILING DATE: 2001-05-14
    PRIOR APPLICATION NUMBER: US 60/204,445
    PRIOR PILING DATE: 2000-05-15
    NUMBER OF SEQ ID NOS: 16
    SOFWARE: Patentin Ver. 2.1
    SEG ID NOS: 16
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       TYPE: PRT
ORGANISM: Homo sapiens
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| APPLICANT: CAO, Liang |
| APPLICANT: CAO, Liang |
| APPLICANT: LU, Jianming |
| APPLICANT: LLORENTE, Isabel |
| TITLE OF INVENTION: Novel Cell-Based Assays Employing Voltage and Calcium Dyes |
| TITLE OF INVENTION: NOVEL Cell-Based Assays Employing Voltage and Calcium Dyes |
| TITLE OF INVENTION: NOVEL COLO-US |
| TITLE OF INVENTION: NOVEL COLO-US |
| CURRENT APPLICATION NUMBER: US 60/589,012 |
| PRIOR PELING DATE: 2004-01-0 |
| PRIOR PELING DATE: 2004-030 |
| PRIOR PELING DATE: 2002-030 |
| PRIOR PELING DATE: 2002-030 |
| PRIOR PELING DATE: 2001-0-30 |
| PRIOR PELING DATE: 2001-10-26 |
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US-09-855-828-13
US-09-855-828-13
Sequence 13, Application US/09855828
Publication No. US20040137433A1
GENERAL INFORMATION:
TAPLICANT: Creech, Christopher D.
APPLICANT: ICAgen, Inc.;
TITLE OF INVENTION: CMG38: A Novel Cyclic Nucleotide-Gated Cation Channel
FILE REFERENCE: 018512-006010US
CURRENT APPLICATION NUMBER: US/09/855,828
CURRENT APPLICATION NUMBER: US 60/204,445
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 809
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                                                                                                                    VPQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVR
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                                                    LFILHINACVYYWASNYEGIGTTRWVYDGEGNEYLRCYYWAVRTLITIGGLPEPQTLFEI
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Pred. No. 1.4e-300;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 808; Conservative 0
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US-09-855-828-13
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ORGANISM: Homo sapiens
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LOCATION: (1). (1245)
OTHER INFORMATION: CNGB1
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                                                                                                     Length 615;
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                                                                                                  76.0%; Score 3217; DB 5; L
100.0%; Pred. No. 1.1e-226;
tive 0; Mismatches 0;
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Publication No. US20050221426A1

GENERAL INFORMATION:
APPLICANT: YAO, Yong
APPLICANT: CAO, Liang
APPLICANT: LLORENTE, 18abel
TITLE OF INVENTION: Novel Cell-Based Assays Emp;
FILE REFRENCE: 062614-5002-US
CURRENT APPLICATION NUMBER: US/10/978, 282
CURRENT FILING DATE: 2004-11-01
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEEVLTIEVKEKAKO 809
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)...(615)
; OTHER INFORMATION: CNGB3
US-10-978-282-14
                                                                                                 Query Match 76.0
Best Local Similarity 100.
Matches 615; Conservative
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46.1%; Score 1952; DB 5;
Best Local Similarity 46.4%; Pred. No. 1.3e-133;
Matches 405; Conservative 121; Mismatches 237;
PRIOR FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 10/087,217
PRIOR PILING DATE: 2002-03-04
PRIOR FILING DATE: 2002-03-04
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 1245
TYPE: PRT
ORGANISM: HOMO SADIENS
FEATURE:
CORGANISM: MISC FEATURE
CORGANISM: MISC FEATURE
COAPTION: (1) 71245
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574 GPDGTKVLVTLKAGSVFGEISLL 413 GPDGKSVLVTLKAGSVFGEISLL 413 SPDGKSVLVTLKQKAKTAEAT	RESULF 6 US-11-097-143-26427 Sequence 26427, Application US/11097143 Publication No. US20050208558A1 GENERAL INFORMATION: APPLICANT: Venter, J. Craig APPLICANT: Venter, J	APPLICATION TELING DATE: APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION AP	SSOTUMARE: FastSEQ for Windows Version 4.0
Qy 729 ENEDKGKE-NEDKDKGREPERKPLDRPECTASPIAVEEEPHSVRRTVLP 776 Db 1165 DQHTHFKEAATDPPAFRTPPEPPGSPPSSPPPASLGRPEGEEEGPA-EPEEHSVR 1218 Qy 777 RGTSRQSLIISMAPSAEGGEEVLTEVKEKAKQ 809 Db 1219ICMSPGPEPGEDLSVKMPEEREE 1242 RESULT 5 US-10-450-763-57830 ; Sequence 57830 ; Sequence 57830 ; Result 5 US-10-450-763-57830 ; Publication No. US20050196754A1 ; APPLICANT: Hyseq, Inc ; APPLICANT: Hyseq, Inc ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES ; FILE REFERENCE: 790CTP3/US ; CURRENT APPLICATION NUMBER: US/10/450,763	PRIOR APPLICATION NUMBER: 2003-06-11 PRIOR APPLICATION NUMBER: 09/540,217 PRIOR PELING DATE: 2001-03-30 PRIOR PELING DATE: 2000-03-31 PRIOR PELING DATE: 2000-03-31 PRIOR PILING DATE: 2000-06-23 NUMBER OF SEQ ID NOS: 60736 SEQ ID NO 57830 LENGTH: 652 TYPE: PRT ORGANISM: Homo sapiens FRATURE: NAMEKEY: DOMAIN LOCATION: (387)(411) OTHER INFORMATION: Cyclic nucleotide-binding domain proteins domain identified OTHER INFORMATION: OF 14 7781. OTHER INFORMATION: OF 14 7781.	FEATURE: NAMENCES: NAMENCE	DD 53 †DLMÝVÍMLPFÝVMÁMNÍMUKALÍPVKHAFÞÝVÍTÞDINHHTILMDÝLÖLITYFOLTI12 QY 274 RLQFVRGGDITUDSNELRKHYRTSTKFQLDVSIIPFDICYLFFGFNPMFRANRHLKYTS 333

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Employing Voltage and Calcium Dyes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 KLPNSIDSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIY 264
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                                                       Length 644;
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24.9%; Score 1052.5; DB 5; Length
Best Local Similarity 38.6%; Pred. No. 5.6e-68;
Matches 227; Conservative 97; Mismatches 205; Indels
                                                                                             Indels
, OTHER INFORMATION: Xaa = X or * as defined in Table US-10-450-763-35825
                                                                                                                                                                                                                                                                                                                                                                    774 VLPRGISRQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809
                                                                                                                                                                                                                                                                                                                                                                                          609 VLPRGTSRQSLIISMAPSAEGGEEVLTIEVKEKAKO 644
                                                       25.7%; Score 1088; DB 5;
100.0%; Pred. No. 9.9e-71;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1). (821)
; OTHER INFORMATION: Xaa = any naturally occurring
US-10-978-282-19
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APPLICANT: CAO, Liang
APPLICANT: LU, Jianming
APPLICANT: LLORENTE, Isabel
TITLE OF INVENTION: Novel Cell-Based Assays
FILE REFERENCE: 062614-5002-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/978,282
CURRENT FILING DATE: 2004-11-01
PRIOR APPLICATION NUMBER: US 60/589,012
PRIOR FILING DATE: 2004-07-20
PRIOR PILING DATE: 2003-10-30
PRIOR PLILING DATE: 2003-04
PRIOR PLILING DATE: 2003-04
PRIOR APPLICATION NUMBER: US 60/330,663
PRIOR PLILING DATE: 2002-03-04
PRIOR PLILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 821
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                                                                             Best Local Similarity 100.
Matches 216; Conservative
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                                                           Query Match
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LOCATION: (58)..(105)
OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
OTHER INFORMATION: eMATRIX, accession number DM01354V, p-value=1.000e-40,
OTHER INFORMATION: 12.97
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                         ----PNSIDSYTD----RLYLLWLLLVTLA 228
                                               229 YNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSN 288
                                                                                                                       289 ELRKHYRTSTKFQLDVASIIPFDICYLFFGFNPMF-RANRMLKYTSFFEFNHHLESIMDK 347
                                                                                                                                                                                                     348 AYIYRVIRTTGYLLFILHINACVYYWASNYEGIGTTRWVYDGEGNEYLRCYYWAVRTLIT 407
                                                                                                                                                                                                                                                                           596 PHFVRVAKTLTYMLYMIHITAALYYAXSDYQGLGQNRWVFSGKGHPYVRCFAFATKTATS 655
                                                                                                                                                                                                                                                                                                                                  408 IGGLPEPOTLFEIVFOLLNFFSGVFVFSSLIGOMRDVIGAATANONYFRACMDDTIAYMN 467
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APPLICANT: Hyeeq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR PILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CUSTOM

SEQ ID NO 35825

LENGTH 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35825, Application US/10450763; Publication No. US20050196754A1; GENERAL INFORMATION:
                         FKVKKMPLTEYLKRIKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: (1)...(644)
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US-10-450-763-35825
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Db 224 SPSPIWFVDCDDPNLTSVLERPEDTENNNYLRQQLKCTWMFEMLDQPLPMGQNGKIEVTS 283	303	284 EEEEEEMAGDIKTLNHCKWKKEEDISGKKLEDEGIEKENLATLEKIRKTÇSÇGHLNVMMC	Db 344 LGSGETTKPRNSGSTGRRKESKQLKAGSQREWLQVQ1QTIGILMSEKAELWTALYTQHA 403	Qy 303DVASIIPF	311DICYLFEGENPMFRANRMLKYTSFFE	Db 464 TWQNDLTTISHAVFQNGELKEQLAKLQTGFMKLNNENMEITSTPQSEQHIKKEPSEKIAN 523	Qy 337	340 HLESIMDKAYIYR	DD 584 FMELMQEKVDLKEQMEKLERRCIQLSGETDVIIHHTVPELEVSAEDVAPEGIHQQPGPCO 643	Oy 353	Qy 353VIRTTGYLLFILHINACYYYWASNYEGIGTTRWYYDGEGNE 393 	RESULT 10 US-10-189-507-11 ; Sequence 11, Application US/10189507 ; Publication No. US20030228633A1	; GENERAL INFORMATION: ; APPLICANT: ZOLLER, MARK	; APPLICANT: XU, HONG ; APPLICANT: STASZEWSKI, LENA ; APPLICANT: MOYER, BRYAN	; APPLICANT: PRONIN, ALEXY ; APPLICANT: ADLER, JON ELLIOT ; APPLICANT: SERVANT, GUY	; APPLICANT: CALLAMARAS, NICHOLAS ; TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC ; TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST ; TITLE OF INVENTION: CPITS AND MES TRUBEDED IN CRIT BASED ASSAVE TO IDENTIFY	; IIILE OF INVENTION: CELLS AND USE INCELL BASED ASSAIS IO IDENIIFI ; TITLE OF INVENTION: SMELL MODULATORS ; FILE REFERENCE: 078003-0291567 ; CIRRENT APPLICATION NIMBER: US/10/189,507	CURRENT FILING DATE: 2003-02-12; PRIOR APPLICATION NUMBER: 60/303,140 ; PRIOR PILING DATE: 2001-07-06; PRIOR APPLICATION NUMBER: 60/33,154	HIOR FILING DATE: 2001-12-10 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin Ver. 2.1	1 37	; TYPE: PRT ; ORGANISM: Homo sapiens US-10-189-507-11	Query Match 21.4%; Score 906; DB 4; Length 237; Best Local Similarity 72.8%; Pred. No. 5.2e-58; Matches 171; Conservative 29; Mismatches 35; Indels 0; Gaps 0;	NFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVO 47 - - :	
Db 376 RLNRLLKFSRLFEFFDRTETRTNYPNIFRIINLVLYILVIIHWNACVYYAISKYIGFGTD 435	Qy 384 RWVYDGEGNEYLRCYYMAVRTLITIGGLPEPQTLFEIVPOLLNFFSGVFVFS 435	130 INVINGIGUEEFGKLAKEILISLINGILILLIGEIFFFVIDEEIVFVVVUFLLGGVEFF	436 SILGGMEDVIGARITANQNYFRACMDTIATRNNYSIPELYGKKVYFYKYEYTWOSGMEDE 495	Qy 496 SDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKG 555	EIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGGGNRRTANVVAHG	Db 616 DIGKEMYIİKEĞKLAVVADXDĞVTQLVVLSAĞSVFGEİSILNIKĞSKSĞNRRTANIVSLĞ 675	OY 613 FANLLTLDKKTLQEILVHYPDSERILMKKARVLLKQKAKTAEATPPRKDLALLFPPKEET 672 1	673 PKLFKTLIGGTGKASLARLLKLKREQAAQKKENSE	/36	QY 708 GGEEGGRENDEDKQKENEDKGKENEDKDREPEEKPLDRPE 755 Db 796 GXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	RESULT 9 US-10-450-763-42328 ; Sequence 42328, Application US/10450763	; Publication No. US20050196754A1 ; GENERAL INFORMATION: ; APPLICANT: Hyseq, Inc. ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES ; FILE REFERENCE: 790C1P3/US	; CURRENT APPLICATION NUMBER: US/10/450,763 ; CURRENT FILING DATE: 2003-06-11	; PRIOR APPLICATION NUMBER: PCT/USO1/08631 ; PRIOR FILING DATE: 2001-03-30 ; PRIOR APPLICATION NUMBER: 09/540,217	; PRIOR FILING DATE: 2000-03-31 ; PRIOR APPLICATION UNDBER: 09/649,167 ; PRIOR FILING DATE: 2000-08-23) NUMBER OF SEQ ID NOS: 60736) SOFTWARE: Cletom) SEQ ID NO 42328 : LENGTH: 747	TYPE: PRT ; ORGANISM: Homo sapiens US-10-450-763-42328	Query Match 22.6%; Score 955; DB 5; Length 747; Best Local Similarity 32.8%; Pred. No. 6.8e-61; Matches 231; Conservative 17; Mismatches 34; Indels 422; Gans 6:	112 NSPQNKPPAAPVINEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVP 17	44	QY 172 PVKESDDKPTEHYYRLAWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLAYNW 231	Qy 232 NCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDII 284		

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APPLICANT: PRONIN, ALEXY
APPLICANT: PRONIN, ALEXY
APPLICANT: ADLER, JON ELLIOT
APPLICANT: ADLER, JON ELLIOT
APPLICANT: CALLAMARAS, NICHOLAS
TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
TITLE OF INVENTION: SYRELL MODILATORS
TITLE OF INVENTION: SYRELL MODILATORS
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TITLE OF INVENTION: SYRELL MODILATORS
TITLE OF INVENTION SYRELL MODILATORS
TITLE OF INVENTION SYRELL MODILATORS
TITLE OF INVENTION NUMBER: 60/303,140
PRIOR PELICATION NUMBER: 60/303,140
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/337,154
PRIOR PELING DATE: 2001-12-10
SOFTWARE: PARENTIN VET: 2.1
SOFTWARE: PARENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 KRVRTWYBYTWDSQRMLDBSDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDM 536
                                                                      1 LFEIVFQLLNYFTGVFAFSVMIGQMRDVVGAATAGQTYXRSCMDSTVKYMNFYKIPRSVQ 60
1 LFEIVFOLLNYFIGVFAFSVMIGQMRDVVGAATAGQTYYRSCMDSTVKYMNFYKIPKSVQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ZOLLER, MARK
APPLICANT: XU, HONG
APPLICANT: STASZEWSKI, LENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 72.39
Matches 170; Conservative
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US-10-189-507-7
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Sequence 75, Application US/09842758; Publication No. US20030083244A1; GENERAL INFORMATION:

RESULT 12 US-09-842-758-75

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APPLICANT: Retranded, alerie A
APPLICANT: Statech, valetie A
APPLICANT: Statech, valetie A
APPLICANT: Statech, valetie A
APPLICANT: Statech Statech Alerie E
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Silos-Santiago, Immacculada
APPLICANT: Silos-Santiago, Immacculada
APPLICANT: Venkateswarlu, Karicheti
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REPRENENCE: MPTO-0.1291RNM OMNI
CURRENT APPLICATION NUMBER: US/10/345,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 WNACIYFAISKFIGFGTDSWVYPNISIPEHGRLSRKYIYSLYWSTLTLTTIGETPPPVKD 375
                                                                                                                                                                                                                                                                                                                                                                                   137 AKCNINTSNNTEEEKKTKKKDAIVVDPSSNLYYRWLTAIALPVFYNWYLLICRACFDELO
                                                                                                                                                                                                                                                                                                                                               -----TEYLKRIKLPNSI-DSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQT
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     NEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTPVTSEEPHTN1QDKLSKKNSSGDL,TTNP
                                                                                                                   DPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPAAPVINEYADAQLHNLVKRMRQRTAI.Y
                                                                                                                                                                         44 ---SVLQP-GIAMETRGLADSGQGSFTGQ------GIARLSRLIFLLRRWAARH
                                                                                                                                                                                                                                 147 KKKLVEGDLSSP-----EASPQTAKPTAVPPVKESDDKPTEHYYRLLWFKVKKMPL
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PRIOR FILING DATE: 2002-01-18
PRIOR PELLING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/365,041
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                                                        5 NTQYSHPS----
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US-10-345-680-26
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                                                     VHHQDQGPDSFPDRFRGAELKEVSSQESNAQANVGSQEPADRG-----RSAW-----PL 136
                                                                                                                -----TEXLKRIKLPNSI-DSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQT 246
                                                                                                                                                             AKCNTNTSNNTEBEKKTKKKDAIVVDPSSNLYYRWLTAIALPVFYNWYLLICRACFDELQ 196
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TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel FILE REFERENCE: 018512-006010US
CURRENT APPLICATION NUMBER: US/09/855,828
CURRENT FILING DATE: 2001-05-14
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 694
                                                                                                                                                                                                                                                            SEYLMIMIVLDYSADVLYVLDVL-VRARTGFLEQGLAVSDTNRLWQHYKTTTQFKLDVLS
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KKKLVEGDLSSP-----EASPQTAKPTAVPPVKESDDKPTEHYYRLLWFKVKKMPL
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US-09-855-828-14
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US-09-855-828-14
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FILE OF INNENTION: NOWEL PROTEINS AND NUCLEIC ACIDS ENCODING SAFE, FILE REFERENCE: 15966-783 CIPI, CURRENT APPLICATION NUMBER: US/10/174,333
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 60/194,614
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
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TLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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20.1%; Score 850; DB 4; Length 694;
Best Local Similarity 30.0%; Pred. No. 3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 10
       703 KENSEGGEE---EGKENEDKQKENEDKQK 728
                                                                           667 SOVKGGGDKPLADGEVPGDATK-TEDKÓQ 694
                                                                                                                                                                                                                                                         Sequence 75, Application US/10174333 Publication No. US20040029220A1 GENERAL INFORMATION:
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Spytek, Kimberly A.
Majunder, Kumud
Tchernev, Velizar T.
Padigaru, Muralidhara
Patturajan, Meera
Burgess, Catherine E.
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Anderson, David W.
Guo, Xiaojia (Sasha)
Li, Li
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Fernandes, Elma R.
Gerlach, Valerie
Malyankar, Uriel M.
Boldog, Ferenc L.
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Taupier, Raymond J.
Grosse, William M.
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Smithson, Glennda
Rastelli, Luca
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PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/374,063
PRIOR PILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/403,468
PRIOR FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-08-17
PRIOR FILING DATE: 2002-09-27
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LENGTH: 694
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                                                                                                                                                         SEYLMLWLDYSADVLYVLDVL-VRARTGFLEQGLMVSDTNRLWQHYKTTTQFKLDVLS 255
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                                          87
                                                                          -----GIARLSRLIFLLRRWAARH
                                                                                                       -----TEYLKRIKLPNSI-DSYTDRLYLLWLLLVTLAYNWNCWFIPLRLVFPYQT
                                                                                                                                               ADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVAS
------RTHLKVK----TSDRDLNRAENGLSRAHSSSEETS--
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                                     44 ---SVLQP-GIAMETRGLADSGQGSFTGQ-
NTQYSHPS-
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Sequence 7, Appli
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Sequence 312, Appl
Sequence 912, Appl
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Match Length DB
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Perfect 1
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Sequence 19, Application US/10613744

Publication No. US20050272093A1

GENERAL INFORMATION:

APPLICANT: MacKinnon, Roderick

APPLICANT: The Rockefeller University

TITLE OF INVENTION: Assays for Screening Compounds Which Interact With

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof

FILE REFERENCE: 018512-002901US

FILE REFERENCE: 018512-002901US

CURRENT FILING DATE: 2003-07-03

PRIOR PELICATION NUMBER: US 09/045,529

PRIOR APPLICATION NUMBER: US 09/045,529

PRIOR PELING DATE: 1999-03-20

PRIOR PAPLICATION NUMBER: WO PCT/US99/06307

PRIOR PLING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 19

LENGTH: 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                         13, Appl
47, Appl
862, App
17, Appl
1110, Ap
94, Appl
20, Appl
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127,
600,
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19.3%; Score 818.5; DB 6;
Best Local Similarity 30.0%; Pred. No. 1.2e-51;
Matches 221; Conservative 128; Mismatches 262;
                       US-10-485-517-401
US-10-485-517-401
US-10-485-517-208
US-10-745-717-206
US-10-821-234-1657
US-10-921-545-13
US-10-982-545-13
US-11-089-551A-47
US-11-089-551A-47
US-11-113-837-17
US-11-113-837-17
US-11-113-837-17
US-11-188-743-20
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US-10-873-528-163
US-10-485-517-127
US-10-995-561-600
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; ORGANISM: Homo sapiens
US-10-613-744-19
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GENERAL INFORMATION:
APPLICANT: MacKinnon, Roderick
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Channel Proteins, and Uses Thereof
TITLE OF INVENTION: Channel Proteins, and Uses Thereof
FILE REFERENCE: 018512-002901US
CURRENT FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: US/09/275,252
PRIOR FILING DATE: 1999-03-20
PRIOR PLING DATE: 1999-03-20
PRIOR PPLICATION NUMBER: US 09/045,529
PRIOR PPLICATION NUMBER: US 09/054,347
PRIOR PPLICATION NUMBER: WO PCT/US99/06307
PRIOR PLING DATE: 1999-03-20
PRIOR PLING DATE: 1999-03-22
PRIOR PLING DATE: 1999-03-22
PRIOR PLING DATE: 1999-03-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLK
                                                                                                                                                                     IYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEYL,
                                             FQLLNFFSGVFVFSSLIGQMRDVIGAATANONYFRACMDDTIAYMNNYSIPKLVQKRVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 EEPHTNIQDKLSKKNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 PTEHYYRLLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLY----LLWLLLVTLAYNWNCWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 IPLRLVFPYQTADN-----IHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 TPYSAAFLLKETEEGPPATECGYACOPLAVVDLIVDIMFIVDIL-INFRTTYVNANEEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 D-SNELRKHYRTSTKFQLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFFFNHHLESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 NKVKPIGENNENEQ-----SSRRNEEGSHPSNQSQQTTAQEENKGEEKSL-KTKSTPVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 NHVAGLGPAEERRALVGPGSPPRSAPGQLPSPRAH--SLNPDASGSSCSLARTRSRESCA
                                                                                                                                                                                                                                        542 SVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGEISLLAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 SVRRASSADDIEAMRAG---VLPPPPRHAS--TGA-----MHPLRSG----
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.larity 21.1%; Pred. No. 2.8e-15;
Conservative 129; Mismatches 286;
                                                                                                                                                                                                                                                                                                                                     601 --GNRRTANVVAHGFANLLTL 619
                                                                                                                                                                                                                                                                                                                                                                                  240 KMGNRRTANIRSLGYSDLFCL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 12, Application US/10613744; Publication No. US20050272093A1
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SOFTWARE: PatentIn Ver. 2.1
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US-10-613-744-12
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nes 146; Conserv
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SEQ ID NO 12
LENGTH: 1159
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Best Local S
Matches 146
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APPLICANT: MacKinnon, Roderick
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof
FILE REFERRINCE: 018512-002901US
CURRENT APPLICATION NUMBER: US/09/275,252
PRIOR PLILNG DATE: 1999-03-24
PRIOR PLILNG DATE: 1999-03-24
PRIOR PLILNG DATE: 1999-03-22
PRIOR APPLICATION NUMBER: US 09/054,347
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR PLILNG DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 261
                                               T--MVIARACFDELQSDYLEYWLILDYVSDIVYLIDM-FVRTRTGYLEQGLLVKEELKLI 237
                                                                                                                                                                  297
                                                                                                                                                                                                             YRVIRTTGYLLFILHINACVYYWASNYEGIGTTRWVY----DGE----GNEYLRCYYWAV 402
                                                                                                                                                                                                                                           358 LTLTTIGETPPPVRDSEYVFVVVDFLIGVLIFATIVGNIGSMISNMNAARAEFQARIDA1 417
                                                                                                                                                                                                                                                                                                                                                                                                             522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 VYYWASNYEGIGTTRWVY----DGE----GNEYLRCYYWAVRTLITIGGLPEPQTLFEIV 421
                                                                                                                                                                                                                                                                                                            RTLITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDT 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKARVLLKQKA----KTAEATPPRKDLALLFPPKEETPKLFKTLLGGTGKASLARLL--- 692
                    NCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                    537 VLSDGSTFGEISILNIKGSKAGNRRTANIKSIGYSDLFCLSKDDLMEALTEYPDAKTMLE
                                                                                                                                         IAYMNNYSI PKLVQKRVRTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKV
                                                                                                              KHYRTSTKFQLDVASIIPFDICYLFFGFN-PMFRANRMLKYTSFFEFNHHLESIMDKAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/10613744
Publication No. US20050272093A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-613-744-18
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Query Match Best Local Matches 9

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Sequence 7, Application US/10613744

Sequence 7, Application US/10613744

Publication No. US20050272093A1

GENERAL INFORMATION:

APPLICANT: MacKinnon: Roderick

APPLICANT: The Rockefeller University

TITLE OF INVENTION: Assays for Screening Compounds Which Interact With

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation

TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof

FILE REFERENCE: 10812-00291US

CURRENT FILING DATE: 1999-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-04-02

PRIOR FILING DATE: 1998-04-02

PRIOR FILING DATE: 1998-04-02

PRIOR FILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 EOWFNOYLHSLYWSIITMTTIGYGDITPONLRERVFAVGMALSAVGVFGYSIGNINSIYA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 EKPTGFQKGQHFLNQTLLIPLRKTKLLKIYCGNQKLIMRPESLASIWWNIYILTIL--- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 IVDSNELRKHYRTSTKFQLDVASIIP-----FDICYLFFGFNPMFRANRMLKYTSFFEF 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 IENRYQIAKNYLRSS-FFFDIFVVIPYFISLRFDLQYLDLVI-----ILKVFQITKF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 SRNLFDRLELTAIQIVIVDLVKLGYTILAAAHFSACIWFLVGSTGNPNDTSWIKAQNIEN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EG--NEYLRCYYWAVRTLITIG-GLPEPQTLFEIVFOLLNFFSGVFVFSSLIGOMRDVIG 446
                                                                                                                                                                                                                384 LVSEMKAEYFPPKEDVILQNEAPTDFYILVNGTADLVDVDTGTESIVREVKAGDIIGEIG 443
                                                                                          FQLLNPFSGVFVFSSLIGQMRDVIGAATANQNYFRACMDDTIAYMNNYS----IPKLVQK 477
                                                                                                                        RV--RTWYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYD 535
                                                                                                                                                                                                                                                                                MLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLV-TLKAGSVFGEIS 594
----ASNYEGIGTTRWVYDGEGNEYLRCYYWAVRTLITIG-GLPEPOTLFEIV 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 DKPT----EHYY-RLLWFKVKKMPLTEYL----KRIKLPNSIDSYTDRLYLLWLLLVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 AYNWNCWFIPLRLVFPYQTADNIHYWLIADIICDIIYLYDMLFIQPRLQF----VRGGDI
                             :| : | | : | | | : : 444 VLCY----RPQLFTVRTKRLCQLLRMNRTTFLNIIQANVGDGTIIMNNLLQHLKE 494
                                                                                                                                                                                                                                                                                                                                                                           595 LLAAGGGNRRTANVVAHGFANLLTLDKKTLQEILVHYPDSERILMKKARVLLKO 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.7%; Score 282.5; DB 6; Best Local Similarity 23.3%; Pred. No. 3.8e-13; Matches 118; Conservative 95; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Paramecium tetraurelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-613-744-7
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CURRENT APPLICATION NUMBER: US/10/613.744
CURRENT FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: US/09/275,252
PRIOR APPLICATION NUMBER: US 09/045,529
PRIOR PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR PILING DATE: 1998-03-22
PRIOR PLING DATE: 1999-03-22
NUMBER OF SEC ID NOS: 42
SOFTWARE: Patentin Ver: 2.1
SEQ ID NOS: 42
SEQ ID NOS: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 ADIICDIIYLYDMLFIQPRLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFD---- 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 ICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAYIY-RVIRTTGYLLFILHINACV 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFFAIDIIMTFFVGYLDKSTYL----IVDDRKQIAFKYLRSW-FLLDLVSTIPSEAAMR 151
                                                                                                                                                                                                                                                                                                                                                                                          ||| : |:: | | ::| | 761 THAPPGDTLVHAGDLLTALYFISRGSIEIL---RGDVVVAILGRWDIFGEPLALYARPG- 816
                                                                                                       422
                                                                                                                                                                                               423 QLLNFFSGVFVFSSLIGOMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTW 482
                                                                                                                                                                                                                                                                                                           641 SICVMLIGSLMYASIFGNVSAIIQRLYSGTARYHTQMLRVREFIRFHQIPNPLRQRLEEY 700
                                                                                                                                                                                                                                                                                                                                                            483 YEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVDLFKGCDTQMIYDMLLRLKS 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                       543 VLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLVTLKAGSVFGE-ISLLAAGGG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---SEELIGL 523
                                                                                                                                                                    GTTRWV------YDGEG-----NEYLRCYYWAVRTLITIG-GLPEPQTLFEIVF
                                                                            MDKAYIYRVIRTTGYL------LFIL-----HINACVYYWASNYE-----GI
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484 SHPGRIAVHYFKGW-FLIDMVAAIPFDL--LIFGSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 NRRTANVVAHGFANLLTLDKKTLQEILVHYPD 633
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Publication No. US20050272093A1
GENERAL INFORMATION:
APPLICANT: MacKinnon, Roderick
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                                                                           504 TIVOLALAIDVNFSIISK----VDLFKGCDTQMIYDMLLRLKSVL----YLPGDF---- 550
                                                                                                                 442 KOLAEEMKIDTNMKLIOKNSFLVNNFS-----EQFLISLSKVLIEEKYVPESTIYLVK 494
                                                                                                                                                           ---VCKKGEIGKEMYIIKHGEVQ----VLGGPDGT-KVLVTLK-AGSVFGEISLLAAGGGN 602
                                                                                                                                                                                            495 LINILQQNDPSNYLYILSNGSLSFYITLNNKQQTIKVLETIKNEGQAFGVLEFFQS---Q 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 MFRANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGYLLFILHINACVYYWASNYEGIG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLLKTLPTTVQLALAI----DVNFSIISKV---DLFKGCDTQMI---YDMLLRLKSVL-- 544
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447 AATANQNYFRACMDDIIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDESDLLK---TLP 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 TTRWVYDGEGNEYLRCYYWAVRTLITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.1%; Score 131.5; DB 7; Length 3375;
21.3%; Pred. No. 0.29;
tive 66; Mismatches 198; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chiang, Wen
APPLICANT: Strasburg, Gale
APPLICANT: Strasburg, Gale
APPLICANT: Linz, John
TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
FILE REFERENCE: MSU-09308
CURRENT APPLICATION NUMBER: US/11/044,111
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                        603 RRTANVVAHGFANLLTLDKKTLQEIL 628
                                                                                                                                                                                                                                                                 S52 AYQVSCKSNQFSYVLKIDKSQFMEII 577
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Publication No. US20050272362A1
GENERAL INFORMATION:
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; ORGANISM: Meleagris gallopavo
US-11-044-111-23
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                                                                                                                                                                                                                                                                                      APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 05/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PLIING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2900
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QDEPPKDEGAEVEDNKDGNSGESSENKPSDDEPEGTSDEEKPDDAPKPDDKPEETPE-TP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   705 NSEGGEEGKENEDKQ----KENEDKQKENEDKGKENEDK-DKGREPEEKPLDRPECTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: synthetic;
CTHER INFORMATION: amino acid sequence
US-10-793-626-2900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence: synthetic; ) OTHER INFORMATION: amino acid sequence US-10-793-626-3226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 2.9%; Score 124; DB 6; Length 44 Local Similarity 27.9%; Pred. No. 0.067; hes 48; Conservative 24; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  662 LALLFPPKEETPKLFKTLLGGTGKASLARLLKLKREQAAQKKE----
                                                          2871 ------ PPPEGAFEFWTELEVQ 2886
774 VLPRGTSRQSLIISMAPSAEGGEEVLT-IEVK 804
                                                                                                                                                                                                Sequence 2900, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                           US-10-793-626-2900
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; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912
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US-10-821-234-1573
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                                                                                                                                                                                                                                                                                                                                                                                     JAPELICANT: MacKainnon, Roderick
APPLICANT: MacKainnon, Roderick
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof
FILE REFERENCE: 018512-002901US
CURRENT APPLICATION NUMBER: US/10/613,744
CURRENT FILING DATE: 1999-03-24
PRIOR PILING DATE: 1999-03-24
PRIOR PLILING DATE: 1999-03-20
PRIOR PLILING DATE: 1999-03-22
PRIOR PLILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 38
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 EYLRCYYWAVRTLITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQ 452
                                                                                        705 NSEGGEEEGKENEDKQ-----KENEDKQKENEDKGKENEDK-DKGREPEEKPLDRPECTA 758
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Adarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOPTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 912
                                                                                                             61 QDEPPROEGAEVEDNKOGNSGESENKPSDDEPEGTSDEEKPDDAPKPDDKPETTP-TP
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                                                                                                                                                                          759 SPIAVEE--EPHSVRRTVLPRGTSRQSLIISMAPSAEGGEEVLTIEVKEKAK 808
                                                                                                                                                                                                        22; Indels
    562 LALLFPPKEETPKLFKTLLGGTGKASLARLLKLKREQAAQKKB-
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; Pred. No. 0.013;
13; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                              ; Sequence 38, Application US/10613744; Publication No. US20050272093A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 36.1%;
Matches 22; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 2, Application US/11128572

Sequence 2, Application US/11128572

Publication No. US20050266513A1

GENERAL INFORMATION:

APPLICANT: Boehringer Ingelheim International GmbH

TITLE OF INVENTION: Method for identifying compounds that have the potential to 1nhib;

TITLE OF INVENTION: activity of Myc

FILE REPERENCE: Case 12-0211-PCT

CURRENT APPLICATION NUMBER: US/11/128,572

CURRENT FILING DATE: 2005-05-13

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin version 3.1
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                                                                                                                                                            524 LFKGCDTQMIYDMLLRLKSVLYLPGDFVCKKGEIGKEMYIIKHGEVQVLGGPDGTKVLV- 582
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Publication No. US20050255114A1
Publication No. US20050255114A1
Publication No. US20050255114A1
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tribang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                     469 -YSIPKLVQKRVRT----WYEYTWDSQRMLDESDLLKTLPTTVQLALAIDVNFSIISKVD
                                                          Gaps
                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 VGRLGPSDYFGEIALLM----NRPRAATVVARGPLKCVKLDRPRFERVL 388
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                                                                                                                    426 NFFSGVFVFSSLIGQMRDVIGAATANONYFRACMDDTIAYMNN----
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Query Match 24.0%; Score 116.5; DB 6; Best Local Similarity 24.0%; Pred. No. 0.21; Matches 55; Conservative 29; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25, Mismatches
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25.6%; Pred. No. 9
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Best Local Similarity 25.6*
Matches 33; Conservative
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ORGANISM: Homo sapiens
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.096 TIIEVELTNIQKKYYRAILEKNFSFLS-----KGAGQTNVPNLVNTMMELRKCCNHP--- 1147
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TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Channel Proteins, and Uses Thereof
FILE REFERENCE: 018512-002901US
CURRENT PAPLICATION NUMBER: US/10/613,744
CURRENT PILING DATE: 2003-07-03
PRIOR FILING DATE: 1999-03-24
PRIOR PLICATION NUMBER: US 09/045,529
PRIOR PLICATION NUMBER: US 09/045,529
PRIOR PLICATION NUMBER: US 09/045,529
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1999-03-22
PRIOR PELING DATE: 1999-03-22
NUMBER: US 09/054,347
PRIOR PLING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                       274 RLQFVRGGDIIVDSNELRKHYRTSTKFQLDVASIIPFDICYLFFGFNPMFRANRMLKYTS 333
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                                                                                     813 KEDVDLAKIEEFEQLQASRPDTRRLDRPPSNIWKKIDQSRDYKNGNQLREYQLEGLNWLL 872
                     WL.L. 223
                                                                                                                                                                                                                           ----ILADEMGLGKTIQSITFLYEIL
                                                                                                                                                    224 LVTLAYNW----NCWFIPLRLVFPYQTADNIHYWLIAD-----IICDIIYLYDMLFIQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 GQMRDVIGAATANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRML
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                                                                                                                                                                                                                 873 ----FNWYNRRNC-
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US-10-613-744-39
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Publication No. US20050250717A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BENAYAHU, Dafna
APPLICANT: SHUR, Irina
TITLE OF INVENTION: CHECKATIN REWODELING PROTEIN AS A MARKER EXPRESSED BY STROWAL ITILE OF INVENTION: CELLS, DNA BNCODING SAME, ANTIBODIES THERETO, AND METHODS OF UNRENT FILING DATE: 2004-06-21
CURRENT FILING DATE: 2004-06-21
SUMMER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO SECONDE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF USERVINE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 YAWESSAGGSFTVRIDIGE--PMGRGTKVILHLKEDQTEYLE-----ERRIKEIVK-K 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REQ------GK 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 HSQFIGYPITLFVEKERDKEVSDDEAEBKEDKEERKERKEEKESEDKPEIEDVGSDEEEEK 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 GTKAFMEALQAGA---DISMIGQFGVGFYSAYLVA------EKVTV--ITKHNDDEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577 GTKVLV-TLKAGSVFGEISLLAAGGGNRRTANVVAHGFANLLTLDKKTLQEILVHYPDSE
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                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 2.6%; Score 112; DB 6; Length 635; Best Local Similarity 23.2%; Pred. No. 0.78; Matches 51; Conservative 43; Mismatches 74; Indels
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PL SEQ_Genes Version 1.0
SEQ ID NO 1573
                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 QQNHNDPNTGLAHQPAHQNIGSAGRASPYGSRG------PSPAQRPRTS--GNSGQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | : : | : : | 306 YEIFSEDITRFYIAEIVLAIDAVHXL.------GFIHRDIKPDNILLDRGGHVKLTDF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNSSGDLTTNPDPQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPAAPVINEYADAQLHNL 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LWPKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLAY 229
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                                                                                                                                                                    393 EYLRCYYWAVRTLITIGGLPEPQTLFEIVFQLLNFFSGVFVFSSLIGQMRDVIGAATANQ 452
                                                                                                                                                                                        ENNENEQSSRRNEEGSHPSNQSQQTTAQEENKGEEKSLKTKSTPVTSEEPHTNIQDKLSK
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APPLICANT: Akin, Ali R.
APPLICANT: Bodie, Elizabeth A.
APPLICANT: Bodie, Elizabeth A.
APPLICANT: Burrow, Shirley
APPLICANT: Dunn-Colemen, Nigel
APPLICANT: Ward, MICHEI
APPLICANT: Ward, MICHEI
APPLICANT: Ward, MICHEI
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TITLE OF INVENTION: Regulatable Growth of Filamentous Fungi
FILE REFERENCE: GC68-2
CURRENT FILING DATE: 2005-04-25
PRIOR APPLICATION NUMBER: US 60/276,511
PRIOR APPLICATION NUMBER: US 60/276,618
PRIOR PILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                         Query Match 2.5%; Score 107; DB 6; Length 57; Best Local Similarity 36.1%; Pred. No. 0.069; Matches 22; Conservative 13; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/11113837; Publication No. US20050255513A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 598
TYPE: PRT
ORGANISM: Neurospora crassa
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-39
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Aa876156 DNA encod
Ab119457 Drosophil
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AAS66653
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Jegla TJ WPI; 2002-089847/12. P-PSDB; AAE15982. 9 Creech

New polypeptide, useful for screening for modulators of cyclic nucleotide -gated ion channels, comprises the isolated cyclic nucleotide-gated cation channel 3 beta subunit. Claim 4; Fig 2; 83pp; English

The invention relates to human cyclic nucleotide-gated cation channel 3 beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms cunctional heteromultimers with CNG41 and/or CNG43, two CNG alpha subunits that are expressed in retina. CNG3B polypeptides are useful for screening modulators of CNGs which are useful as contraceptives and for treating various disorders involving cation channels. e.g. vision disorders and male infertiilty. Polynucleotides of the invention are useful for transfection of cells in vitro and in vivo, to correct acquired and inherited genetic defects, cancer and viral infections. Sequences of the invention are useful as reporter molecules in assays and detection systems, to measure changes in cation concentration, membrane potential, current flow, ion flux, transcription, signal transduction, reporter-ligand interactions and second messenger concentrations, in vivo and ex vivo. They are useful to construct models of CNGs in a computer system and for examining expression and regulation of cation channels. The present sequence is a DNA encoding CNG3B protein

Sequence 2757 BP; 946 A; 571 C; 581 G; 659 T; 0 U; 0 Other;

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240 540 GAACAAAGTTCTCGTCGGAATGAAGAAGGCTCTCACCCAAGTAATCAGTCTCAGCAAACC 120 231 ACAGCACAGGAAGAAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC 180 291 351 GATCTGACCACAAACCCTGACCCTCAAAATGCAGCAGAACCAACTGGAACAGTGCCAGAG 300 411 360 471 420 531 480 591 651 ACAGAACATTACTACAGGCTGTTGTGGTTCAAAGTCAAAAAGATGCCTTTAACAGAGTAC 600 9 ACGTCTGAAGAGCCACACACCAACATACAAGACAAAAACTCTCCAAGAAAATTCCTCTGGA 292 ACGICIGAAGAGCCACACCAACATACAAGACAACTCICCAAGAAAATICCICIGGA GATCTGACCACAAACCCTGACCCTCAAAATGCAGCAGAACCAACTGGAACAGTGCCAGAG GCTCCTGTTATAAATGAGTATGCCGATGCCCAGCTACACAACCTGGTGAAAAGAATGCGT GCTCCTGTTATAAATGAGTATGCCGATGCCCAGCTACAACAACCTGGTGAAAAGAATGCGT CAAAGAACAGCCCTCTACAAGAAAAGTTGGTAGAGGGAGATCTCTCCTCACCCGAAGCC 1 ATGITIAAATCGCTGACAAAGTCAACAAGGTGAAGCCTATAGGAGAGAACAATGAGAAT Gaps ; 0 DB 6; Length 2757; 0; Indels Query Match
100.0%; Score 2430;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 61 121 181 352 241 412 481 592 541 301 361 472 421 532

1140 1620 1680 1020 1080 1191 1251 1200 1311 1320 14 11 1380 1500 1611 1560 1011 1071 1371 1491 1551 1731 720 840 900 096 711 771 831 780 891 CTAGAGTCTATAATGGACAAAGCATATATTCTACAGAGTTATTCGAACACTGGATACTTG CAGTTGGATGTCGCATCAATAATACCATTTGATATTTGCTACCTCTTCTTTGGGTTTAAT CTGTTTATTCTGCACATTAATGCCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATT ATGAGAGATGTGTTTTGGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCCTGCATGGAT **ACAGAACATTACTACAGGCTGTTGTGGTTCAAAGTCAAAAAGATGCCTTTAACAGAGTAC** TTAAAGCGAATTAAACTTCCAAACAGCATAGATTCATACACAGATCGACTCTATCTCCTG GATATCATCTACCTTTATGATATGCTATTTATCCAGCCCAGACTCCAGTTTGTAAGAGGA CCAATGTTTAGAGCAAATAGGATGTTAAAGTACACTTCATTTTTTGAATTTAATCATCAC CTAGAGICTATAATGGACAAAGCATATATCTACAGAGTTATTCGAACAACTGGATACTTG crerrrarrcrecacarraarecerererrarracresecrreaacrareaaesaarr GGCACTACTAGATGGGTGTATGATGGGGAAGGAAACGAGTATCTGAGATGTTATTTGG GGCACTACTAGATGGGTGTATGATGGGGAAGGAAACGAGTATCTGAGATGTTATTATTGG GCAGTTCGAACTTTAATTACCATTGGTGGCCTTCCAGAACCACAAACTTTGAAATT **ATGAGAGATGTGATTGGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCCTGCATGGAT** ACTIGGIATGAATATACATGGGACTCTCAAAGAATGCTAGATGAGTCTGATTTGCTTAAG ACTTGGTATGAATATACATGGGACTCTCAAAGAATGCTAGATGAGTCTGATTTGCTTAAG AAAGTCGACTTGTTGTAGATACACAGATGATTTATGACATGTTGCTAAGATTG **TTAAAGCGAATTAAACTTCCAAACAGCATAGATTCATACACAGATCGACTCTATCTCCTG** GTCTTCCCATATCAAACCGCAGACAACATACACTACTGGCTTATTGCGGACATCATATGT GTCTTCCCATATCAAACCGCAGACAACATACACTACTGGCTTATTGCGGACATCATATGT GATATCATCTACCTTTATGATATGCTATTTATCCAGCCCAGACTCCAGTTTGTAAGAGGA GGAGACATAATAGTGGATTCAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAATTT CAGTTGGATGTCGCATCAATAATACCATTTGATATTTGCTACCTCTTCTTTGGTTTAAT GCAGTICGAACTITAATTACCATTGGTGGCCTTCCAGAACCACAAACTITATTTGAAATT GITITICAACICITGAATITITITITICIGGAGITITITGIGITCICCAGITITAATIGGICAG GACACCATTGCCTACATGAACAATTACTCCATTCCTAAAACTTGTGCAAAAGCGAGTTCGG GACACCATTGCCTACATGAACAATTACTCCTAAAACTTGTGCAAAAGCGAGTTCGG ACCCTACCAACTACGGTCCAGTTAGCCCTCGCCATTGATGTGAACTTCAGCATCATCAGC Acceraccaactaccerccagraaccercccarrcarcraactreaccarcarcacc **AAAGTCGACTTGTTCAAGGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTG** 1012 1252 1312 1372 1612 661 772 892 952 1072 1021 1132 1081 1192 1201 1321 1432 1381 1492 1441 1552 1501 1621 601 712 721 832 781 841 901 961 1141 1261 1672 ò g ò 음 ઠે ద ઠ g ò 유 ò g ò g ò g ò g ò g ò g ઠે a δ g ò g ò g ò ద ò 임 ò

영 장 셤 કે 셤 ઠે 셤 ઠે 윱 ò g ð 셤 ò

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping.

C and in recombinant production of (II). The polynucleotides are also used in the production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) are to treat disease states involving (II). (II) is cuseful for generating antibodies against it, detecting or quantitating a cuseful for generating antibodies against it, detecting or quantitating a cupplement. (II) and its binding partners are useful in medical imaging consupplement. (II) and its binding partners are useful in medical imaging consupplement. (II) and its binding partners are useful for treating disorders of involving aberrant protein espression or biological activity. The colonypeptide and polynucleotide sequences have applications in diagnostics, for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and can or oproduce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this coing sequences of the printed specification, but was obtained in celectronic format directly from WIPO at calculation of the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 5457; 103pp; English.
                                                   31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                             Tang YT;
                 30-MAR-2001; 2001WO-US008631
                                                                                                                                                                               2001-639362/73
                                                                                                                                             Liu C,
                                                                                                         (HYSE-) HYSEQ INC
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AAATCCGTTCTCTATTTGCCTGGTGACTTTGTCTGCAAAAAGGGAGAAATTGGCAAGGAA 1791
                                                                                                                                                                                                                                                                             1972 AAAAAGACCCTCCAAGAAATTCTAGTGCATTATCCAGATTCTGAAAGGATCCTCATGAAG
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                                                                      ATGTATATCATCAAGCATGGAGAGTCCAAGTTCTTGGAGGCCCTGATGGTACTAAAGTT
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food supplement, medical imaging, diagnostic, genetic disorder; 88.
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                                                                                                                             GTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAAACCGTCGAACTGCCAATGTGGT
                                                                                                                                                                          1853 GTCAGAAAACAACAGCCTTCTAGCAGGAGGAGGAAAACCGTCGAACTGCCAATGTGGT
                                                                                                                                                                                                                GGCCCACGGGTTTGCCAATCTTTAACTCTAGACAAAAAGACCCTCCAAGAAATTCTAGT
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                                          Length 2516;
Sequence 2516 BP; 1040 A; 548 C; 447 G; 481 T; 0 U; 0 Other;
                                                                                  Indels
                                      Query Match 26.9%; Score 654.4; DB 5; Best Local Similarity 99.1%; Pred. No. 1.5e-133; Matches 658; Conservative 0; Mismatches 6;
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WO200175067-A2 sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                     gene; gene therapy; human diagnostic and therapeutic polynucleotide;
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                                                                                                  GCCACTGGACAGACCTGAATGTACAGCAAGTCCTATTGCAGTGGAGGAAGAACCCCACTC
                                                                                                                                                  2393 AGTIAGAAGGACAGTITIACCCAGAGGGACTICTCGTCAATCACTCATTATCAGCATGGC
AGAGGAAGAAGGAAAAGAAATGAAGATAAACAAAAAGAAAATGAAGATAAACAAAAAGA
                        AAATGAAGATAAAGGAAAAGAAAATGAAGATAAAGATAAAGGAAAGAGAGCCAGAAGAGAA
                                                   AAATGAAGATAAAGGAAAAGAAAATGAAGATAAAGATAAAGGAAGAGAGCCAGAAGAGAA
                                                                                                                           AGTTAGAAGGACAGTTTTACCCAGAGGGACTTCTCGTCAATCACTCATTATCAGCATGGC
                                                                                                                                                                             TCCTTCTGCTGAGGGCGGAGAAGAGGTTCTTACTATTGAAGTCAAAGAAAAGGCTAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wright RJ, Bruns CM, Marjanovic MM, Shen F;
TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Delegeane AM, Pensear IS, Banville SC, Reddy TP;
Blanchard JL, Penser SR, Wang X, Au AP, Geretin EH;
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
G M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
                                                                                                                                                                                                                                                                                                                                                                                           Human diagnostic and therapeutic polynucleotide SEQ ID NO:1506
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2002US-0410260P
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                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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P-PSDB; ABM83979.
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Kwong M,
Shi X,
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12-SEP-2002;
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Stevens KA,
Peralta CH,
Lagace RE, S
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The invention relates to novel diagnostic and therapeutic polynuclectides selected from one of the 2722 sequences defined in the specification, A polynuclectide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynuclectides (dithp) or polypeptides may be

Claim 1; Page; 190pp; English.

gene mapping

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used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorder, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorder, gastrointestinal disorder, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polymucleotide the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from MIPO at www.wipo.int/pct/en/sequences/listing.htm
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Best Local Similarity 64.4%; Pred. No. 6.5e-117;
Matches 867; Conservative 0; Mismatches 480; Indels
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease steless involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess produces the procession of propertice and polynucleotides or other traits to assess produces the procession of produces the produces are produced to a produce of the polynucleotides.
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                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Castle A,

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WPI; 2003-731472/69

2002US-0371134P. 2002US-0371135P. 2002US-0371150P. 2002US-0371413P. 2002US-03736UIP. 2002US-03736UIP.

10-APR-2002; 2 11-APR-2002; 2 19-APR-2002; 2 19-APR-2002; 2 22-APR-2002; 2

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2003US-0442900P

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LOGIC INC

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toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;

toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.

Rattus norvegicus

Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3897

(first entry)

04-DEC-2003

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ADB53355 standard; DNA; 4238 BP.

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Best Local Similarity 64.6
Matches 847; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining intracellular concentration of cyclic nucleotides, useful for identifying, e.g. receptor ligands and enzyme inhibitors, comprises using cells that express a cyclic nucleotide activated ion channel and a
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Length 3236;
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The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sectivity of (11) is useful in gene therapy techniques to restore normal cativity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of supplement. (11) and its binding partners are useful in medical imaging of sites expressing (11). (1) and (11) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cations of mutations and to produce other types of data and products dependent on DMA and to produce other types of data and products dependent on DMA and conding sequences. Assettly-AASS4164 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this coding sequences in the printed specification, but was obtained in the print of the invention.
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Best Local Similarity 94.7%; Pred. No. 1.3e-103;
Matches 536; Conservative 0; Mismatches 30;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cortivity of (II) as useful in gene therapy techniques to restore normal cortivity of (II) to to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations capped and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in parent of the invention. Note: The sequence date for this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01972). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                 developmental biology; cell signalling; insecticide;
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Pred. No. 1.1e-38;
0; Mismatches 665; Indels
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11-JUL-2000; 2000US-00614150
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Sequence 2500 BP; 861 A; 431 C; 525 G; 683 T; 0 U; 0 Other;

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central nervous system; CNS; eye; blood-brain barrier; blood-retina barrier; anglogenesis; revascularisation; retinal pigment epithelium; RPE; neurosensory retina; choroidea; age-related macular degeneration; AMD; diabetic retinopathy; Alzheimer's disease; Parkinson's disease; depression; bipolar disorder; schizophrenia; amnesia; headache; stroke; insomnia; alcohol abuse; anxiety; chronic pain; retinal blastoma; primary retinal detachment.
                                                                                              Cyclic nucleotide gated channel alpha 1 coding sequence.
                                                                                                                                                                                                 gene; cyclic nucleotide gated channel alpha 1
(first entry)
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Homo sapiens.

/*tag= a /product= "Cyclic nucleotide gated channel alpha 1" Location/Qualifiers 25. .2097

WO2003087368-A2

23-OCT-2003.

.6-APR-2003; 2003WO-EP004003

18-APR-2002; 2002EP-00008761.

(LYNK-) LYNKEUS BIO TECH GMBH

Goehring Schloer SH, Drumm K,

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2003-845328/78 P-PSDB; ADD93244.

administering to a subject a composition comprising a compound that modulates a target gene or gene product, outside the blood-brain and/or blood-retina barriers. Treating central nervous system and/or eye disorders comprises

Claim 19; SEQ ID NO 1; 91pp; English

This sequence encodes the human cyclic nucleotide gated channel alpha 1 protein. This cDNA may be targeted in the method of the invention for treating a disorder of the central nervous system (CNS) and/or the eye.

CC Treating a disorder of the central nervous system (CNS) and/or the eye.

The method comprises administering to a subject a composition comprising a compound capable of modulating a target gene or gene product in a compound capable of modulating a target gene or gene product in a designed form to be introduced into the cells or tissue of the CNS or eye blood-brain or blood-retina barriers. The composition is in a cell blood-brain or blood-retina barriers. The application occurring outside the blood-brain or blood-retina barriers. The salso designed for systemic administration or for administration by iontophoresis, or for extrobulbar application or as eye drops. The compound, nucleic acid confected or useful for the preparation of a composition for treating, preventing and/or delaying a disorder of the CNS and/or the eye, e.g. related to angiogenesis and/or necvascularisation, retinal programment of pigment epithelium (RPE), neurosensory retina and/or choroidea and wet age-related macular degeneration (AMD) or diabetic retinopathy. The compound may also be used as a lead compound in drug discovery and preparation of drugs or prodrugs. The nucleic acid molecule and compounds, drugs and prodrugs for the treatment of the disorder mentioned above or for the identification and isolation of downstream genes, which respond to modulation of a gene comprising the nucleic acid molecule or cits encoded gene product. The method is used for diagnosing, preventing continears, headache, stroke, insomnia, alcohol abuse, entirely annesia, headache, stroke, insomnia, alcohol abuse, context anxiety, chronic pain, retinal blastome, primary retinal detachment or context anxiety, chronic pain, retinal blastome, primary retinal detachment or context anxiety contexterior.

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                                                                    Gaps
                                                                    36;
      Length 2500;
                                                                    Indels
DB 10;
   Score 176.4; DB 10;
Pred. No. 1.7e-28;
0; Mismatches 591;
      7.3%;
                                   Best Local Similarity 49.6
Matches 617, Conservative
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                                             1682 AAGGGAGCAAAGCTGGCAATCGAAGAACGCCAATATTAAAAGTATTGGCTACTCAGACC 1741
                                                                                                                                                                                                                                                                                                                                                          1742 TGTTCTGTCTCTCAAAAGATGACCTCATGGAAGCTCTAACTGAGTACCCAGATGCCAAAA 1801
---TACTCTGAAAGCTGGGTCGGTGTTTGGAGAAATC--AGCCTTC
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                                                                                                                                                                                                                                                                                      1847 TTTTAACTCTAGACAAAAAGACCCTCCAAGAAATTCTAGTGCATTATCCAGATTCTGAAA
                                                                                                                                           TAGCAGCAGGAGGAGAAACCGTCGAACTGCCAATGTGGGCCCCACGGGTTTGCCAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATGCTAGAAGAAAAGGGAAGCAAATTTTAATGAAAGATGGT 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; prognosis; gene expression; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1907 GGATCCTCATGAAGAAGCCAGAGTGCTTTTAAAGCAGAAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Breast cancer prognosis marker #427
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The invention relates to isolated polymuclectide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain
reaction (PGN) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polymuclectides are also used
in diagnostics as expressed sequence tags for identifying expressed
genes. (I) is useful in gene therapy techniques to restore normal
activity of (II) or to treat disease states involving (II). (II) is
useful for generating antibodies against it, detecting or quantitating a
polypeptide in tissue, as molecular weight markers and as a food
supplement. (II) and tes binding partners are useful in medical imaging
of sites expressing (II). (I) and (II) are useful in medical imaging
of sites expressing (II). (I) and (II) are useful in medical imaging
of solypeptide and polymucleotide sequences have applications in
diagnostics, forenise, gene mapping, identification of mutentions
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
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                                                                1742 IGTICTGTCTCTCAAAAATGACCTCATGGAAGCTCTAACTGAGTACCCCAGATGCCAAAA 1801
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                                                             83 GCAAACTATCACAAGGACAGAAAACCAAACACGCATGTTCTCACACAACAGCCCACAAA
                                                                                             347 ACAAACCGCCTGCAGCTCCTGTTATAAATGAGTATGCCGATGCCCAGCTACACAACCTGG
                              287 GAACAGTGCCAGAGCAGAAGGAAATGGACCCCGGGAAAGAAGGTCCAAACAGCCCCACAAA
                                                                                                                              143 ACAAACCGCCTGCAGCTCCTGTTATAAATGAGTATGCCGATGCCCAGCTACACGTGC
                                                                                                                                                              TGAAAAGAATGCGTCAAAGAACAGCCCTCTACAAGAAAAAGTTGGTAGAGGGAGATCTCT
                                                                                                                                                                                              rgaaaagaargcgrcaaagaacagcccrcracaagaaaaagrrggragagggarcrcr
 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ 1D NO 5728.
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 Indels
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0; Mismatches
                                                                                                                                                                                                                               CCTCACCCGAAGCCAGCCCACAAACTG 493
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11-JUL-2000; 2000US-00614150.
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178; Conservative
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668 IGCTIGICACICITGCCTATAACTGGAACTGCTGGTTTATACCACTGCGCCTCGTCTTCC 727

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Score 160.6; DB 5; Length 289; Pred. No. 2.6e-25;

6.6%;

Query Match Best Local Similarity

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1076 AGACGGTGATGGCCTCCCTGAAGGCTGGTTCCTATTTTGGCGAGATTAGTATACTCAATA 1135
                                                                                                                                                                                                       TAACTCTAGACAAAAAGACCCTCCAAGAAATTCTAGTGCATTATCCAGATTCTGAAAGGA
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Best Local Similarity 46.8%;
Matches 623; Conservative
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P-PSDB; ADF56501.
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          CATATCAAACCGCAGACAACATACACTACTGGCTTATTGCGGACATCATATGTGATATCA
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New nucleic acid encodes modified olfactory cyclic nucleotide-gated ion channels which exhibit increased sensitivity and specificity for CAMP and are useful to elucidate activities of proteins important in CAMP
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                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid encoding a modified olfactory cyclic nucleotide-gared ion channel, where the channel comprises mutations which together impart increased cAMP sensitivity, decreased nitric oxide sensitivity and decreased calcium-calmodulin sensitivity. The invention is used to elucidate activities of receptors, G-proteins, phosphodiesterases, aden cyclases and other proteins important in cAMP signaling. The present sequence represents modified rat olfactory cyclic nucleotide-gated ion
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                                                                                                                  CTGCGCCTCGTCTTCCCATATCAAACCGCAGACAACATACACATACTGGCTTATTGCGGAC
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BX104558 BX104558 B173622 60335912 BM93877 U1-M-CC0P H53423 YC 86409.71 CR376265 CR376265 AW46556 BD230019A BG304577 f188b05.y A1150392 qf40g11.x CX353216 ssalribb5. DN682911 CGX26-H06 AA317961 EST20020 AA017961 EST20020 AA317961 EST20020 AA317961 EST20020 AA317961 EST20020 AA317961 EST20020 AA317961 EST20020 AA317961 EST20020 AA317961 EST20020 AA069498 xf74607.r CD327412 AGENCOURT CX828690 JG1 CAAK6 BX370500 BX370500 AV605887 AV605887	NTS	linear C CRIPT, partial , Vertebrata; E Primates; Catan Glanowski,S., ,D.M., Civello, nd Cargill,M.	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	395; Indela 0;
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11111111111111111111111111111111111111		DQ04374 Homo sapiens CNGB3 gene, VIR genomic survey sequence. DQ043744.1 G1.66894959 GSS. Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Hominidae; Homo. 1 (bases 1 to 2103) Nielsen, R., Bustamante, C., C Hubisz, M.J., Fledel-Alon, A., White, T.J., Sninsky, J.J., Ac A Scan for Positively Select Chimpanzees (er) PLOS Biol. 3 (6), E170 15689325. Chases 1 to 2103)	Loan bisz, D	imi
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Pan troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                          Hominidae; Pan.

1 (bases 1 to 2103)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.!

Nielsen,R., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,

White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans an
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llarity 75.4%; Pred. No. 0;
Conservative 0; Mismatches 513. T.
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)
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/gene="CNGB3"
/locus_tag="HC10349"
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/clone_lib="RIKEN full-length enriched mouse cDNA libiary"
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Mamanoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kabliwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Oharake,S., Matsuhiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                     Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                                                                                        The RIKEN Genome Exploration Research Group Phase II Team and the ANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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(MGD|MGI:1353562, GB|NM_013927, evidence: BLASTN, 100%,
match=2055)"
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Pred. No. 7.7e-179;
0; Mismatches 252;
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/db_xref="taxon:I0090"
/clone="A430069G05"
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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                                                                                                                                            TTGAAATCCGTTCTCTATTTGCCTGGTGACTTTGTCTGCAAAAAGGGAGAAATTGGCAAG 1677
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                   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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ATAAAGATAAAGGAAGAGCCAGAAGAAGAAGCCACTGGACAGACCTGAATGTACAGCAA
                                                                                                                  CTTCTCGTCAATCACTCATTATCAGCATGGCTCCTTCTGCTGAGGGCGGAGAAGAGGTTC
                                                                                                                                                                             TTACTATTGAAGTCAAAGAAAAGGCTAAGCAATAA 2430
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Plate: 16 row: c column: 03
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                                   122 ATTGGGCAGTTCGAACTTTAATTACTATCGGGGGCCTTCCAGAGCCACAGACTTCATTG 181
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Inote="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from the years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First [57-pgACTAGTTCTAGATCGCGACGCCCC(T)15-3']. Not 1/blunt and inserts were cloned into the Not 1/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)." BF725470 S53 bp mRNA linear EST 05-JAN-2001 bx16c03.yl Human Iris cDNA (Un-normalized, unamplified): BX Homo sapiens cDNA clone bx16c03 5', mRNA sequence. /mol type="mRNA" | /mol type="mRNA" | /mol type="taxon:9606" | /clone="bx16c03" | /clone="bx16c03" | /clone="taxon:pe="tris" | /clone="taxon" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol tris" | /mol Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae; Homo.

1 (Basea 1 to 553)

Wistow, G.J.

Wistow, G.J.

WEIBANK. EST analysis and bioinformatics for ocular genomics Invest. Ophthalmol. Vis. Sci. 41 (2000) In press Contact: Wistow G.Section on Molecular Structure and Function National Eye Institute 6/31, NIH, Betheeda, MD 20892-2740, USA

Fax. 301 496 0078 Length 553; 22.8%; Score 553; DB 2; L 100.0%; Pred. No. 1.1e-117; Query Match Best Local Similarity

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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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 Please contact the RZPD: Ressourcenzentrum, Heubnerwe
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
Location/Qualifiers
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100.0%; Pred. No. 3.2
ive 0; Mismatches
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organism="Homo sapiens"
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email 8. Wiemann@Akfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp686Al695) is available at the RZPD in Berlin.
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                                     GITTATICTGCACATTAATGCCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATTGG
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Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen:
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/tissue type="HeLa cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Pred. No. 5.7e-100;
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 391;
                                                                                                                                                                                                      /organism="Homo sapiens
                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                      Location/Qualifiers
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Best Local Similarity
Matches 712; Conserv
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655 bp mRNA linear EST 26-OCT-2001
BB635459 RIKEN full-length enriched, 0 day neonate thymus Mus
BB635459
BB635459.1 GI:16471509
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Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                               903
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Carninci,P., Shibata,Y., Hayetsu,N., Sugahara,Y., Shibata,K.,
Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., TGGawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       963
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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sequencer. Genome
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10 (11), 1757-1771 (2000)
Konno, H., Fukunishi Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
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TTGAAAATCCGTTCTCTATTTGCCTGGTGACTTTGTCTGCAAAAAGGGAGAAATTGGCAAG
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I (bases 1 to 3444)

Nielsen, K., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.H.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Nublasr, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                        1678 GAAATGIATATCATCAAGCATGGAGAAGTCCAAGTTCTTGGAGGCCCTGATGGTACT 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                              601 --AATGTACATCATCAA-CACGGAGAAGTCCAAGTCCTTGGAGGCCCTGATGGTGCT 654
                                             421 GAGAACCTCCCGACAGCAATGCAGTTGTCTATTGCCCTTGACATAAACTTCAGTATCATC
      AAGACCCTACCAACTACGGTCCAGTTAGCCCTCGCCATTGATGTGAACTTCAGCATCATC
                                                                                       AGCAAAGTCGACTTGTTCAAGGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        677 CTCTTGCCTATAACTGGAACTGCTGTTTATACCACTGCGCCTCGTCTTCCCATATCAAA
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Homo sapiens CNGBl gene, VIRTUAL TRANSCRIPT, partial sequence,
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/organism≃"Homo sapiens"
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/chromosome="16"
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             encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KOndo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Atzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Flease visit our web site (http://genome.gsc.riken.go.jp) for further details.
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thymus"
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Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                        /tissue_type="thymus"
/dev_stage="0 day_neonate"
/lab_host="DH108"
                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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                            BF725469 A17 bp mRNA linear EST 05-JAN-2001 bx16c03.xl Human Iris cDNA (Un-normalized, unamplified): BX Homo sapiens cDNA clone bx16c03 3', mRNA sequence.
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/db_xref="taxon:9606"
/clone="bx16c03"
/tissue_type="lris"
/dev_stage="Adult"
/lab_host="EMDH108"
/clone_lib="Human Iris cDNA (Un-normalized, unamplified):
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 437)

Wistow, G.1, Bernstein, S., Behal, A. and Smith, D.

NEIBANK: EST analysis and bioinformatics for ocular genomics Invest. Ophthalmol. Vis. Sci. 41 (2000) In press

Contact: Wistow G.
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99.3%; Pred. No. 4.3e-89;
iive 0; Mismatches 3;
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6/331, N1H, Bethesda, MD 20892-2740,
Tel: 301 402 3452
Fax: 301 496 0078
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                                                             0; Mismatches 171;
                       DB 2;
                       Score 402.4; DB 2
Pred. No. 1.5e-82
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                       16.6%;
73.9%;
                       Query Match
Best Local Similarity 73.9
Matches 548; Conservative
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/clone="IMAGE:3496015"
/tlssue_type="tumor, gross tissue"
/dev stage="n months"
/lab_host="DH10B"
/clone lib="NCI_CGAP_Mam5"
/note="Organ: mammary; vector: pCMV-SPORT6; Site 1: Sall; Site 2: Not1; Cloned unidirectionally. Primer: Ōiigo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                  CCACCGAAAGAAGAGACACCCAAACTGTTTAAAACTCTCCTAGGAGGCACAGGAAAAGCA 138
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1 (bases 1 to 881)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.
                     AATGTGGTGGCCCACGGGTTTGCCAATCTTTTAACTCTAGACAAAAAGACCCTCCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM8547 row: I column: 08
High quality sequence stop: 774.
                                                       ATTCTAGTGCATTACCAGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGCTTTTA
                                                                                                                                 AAGCAGAAGGCTAAAGACCGCAGAAGCCACCCTCCAAGAAAAGATCTTGCCCTCCTTC
                                                                                                                                                                                                          CCACCGAAAGAAGACACCCAAACTGTTTAAAACTCTCCTAGGAGGCACAGGAAAAGCA
                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
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CGX77-A10.yld-s SHGC-CGX Gasterosteus aculeatus cDNA clone CGX77-A10 5', mRNA sequence.
DN691557
DN691557.1 GI:62046053
                                                                                                                                                                                                   Gasterosteus aculeatus (three spined stickleback)
Sasterosteus aculeatus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomı;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
I (bases 1 to 1455)
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AUTHORS

FEATURES

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CGX07-F03.yld-s SHGC-CGX Gasterosteus aculeatus cDNA clone CGX07-F03.y, mRNA sequence.
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Gasterosteus aculeatus
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Noopterygii, Teleostei, Euteleostei, Nooteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Gasterosteiformes;
Gasterosteidae, Gasterosteus.
1 (bases I to 1377)
1 (bases I to 1377)
2 (bases I to 1377)
3 (chamutz, J. and Myers, R.M.
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                                                                                                                                               AGGCACGCGTACCTCCGTTGTTACTACCACACCCCACTCTGATCAACATCGTG
                                                                                                   AAGGAAACGAGTATCTGAGATGTTATTATTGGGCAGTTCGAACTTTAATTACCATTGGTG
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Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGTGGCCCACGGGTT 1838
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/tissue type="eyes"
/dev stage="adult"
/lab/host="with108 (TIT phage resistant)"
/clone lib="SHGC-GXX"
/clone lib="SHGC-GXX"
/clone lib="SHGC-GXX"
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic Not1 site (first strand primer: 5. GACTAGTTGAAACGCGCGCGCCC(T/25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the Not1 and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:
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q.php#8 The primary_library_was_transformed_and_amplified
in_DH10B (T1 phage_resistant)_bacteria. Clones_available
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             Peichel, C., Balabahdra, S., Grimwood, J., Dickson, M.
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      Kingsley, D.M., Peichel, C., Balabahdra, S., Grimwood, J., Schmutz, J. and Myers, R.M.
Expressed sequence tags from Gasterosteus aculeatus Unpublished (2003)
Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5801
Fax: 650 320 5801
Email: jane@8hgc.stanford.edu
Plate: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Conner Creek sticklebacks, WA USA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from Open Biosystems:
http://www.openbiosystems.com/stickleback"
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High quality sequence stop: 941.
Location/Qualifiers
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/clone="CGX77-A10"
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CGX46-A07.yld-s SHGC-CGX Gasterosteus aculeatus cDNA clone CGX46-A07; mRNA sequence.
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          CAGCATCATCAGCAAAGTCGACTTGTTCAAGGGTTGTGATACACAGATGATTTATGACAT 1607
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Gasterosteus aculeatus
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha, Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.

1 (bases I to 1140)
1 (bases I to 1140)
Schmutz, D. M., Peichel, C., Balabahdra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
Expressed sequence tags from Gasterosteus aculeatus
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                                                           GTTGCTAAGATTGAAATCCGTTCTCTATTTGCCTGGTGACTTTGTCTGCAAAAAGGGAGA
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                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/errain="Conner Creek sticklebacks, WA USA"
/db xref="taxon:69293"
/clone="CGX46-A07"
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Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304,
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Plate: 46
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q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1488 TGATTIGCTTAAGACCCTACCAACTACGGICCAGTTAGCCCTCGCCATTGATGTGAACTT 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTACGAAGGACTCGGATCCAAGTGGGTCTACGACGGAAAGGAAACGCTTATATCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8; Length 1377;
                                                                                                                                                                                                                                                               |mol_type="mRNA"
|strain="Conner Creek sticklebacks, WA USA"
|db_xref="taxon:69293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Open Biosystems:
http://www.openbiosystems.com/stickleback"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 388.8; DB 8; Length
Pred. No. 2.4e-79;
0; Mismatches 324; Indels
                                                                                                                                                                                                                                                                                                                                                                                               (tissue_type="eyes"
dev stage="adult"
dbw bast="DH10B (T1 phage resistant)"
clone_lib="SHGC-CGX"
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                          organism="Gasterosteus aculeatus"
                                                                                                                                                                                                                                                                                                                                                                       'sex="mixed male and female"
                                                                                                                                                        High quality sequence stop: 816.
Location/Qualifiers
                                                Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@shgc.stanford.edu
Plate: 07
                                                                                                                                                                                                                                                                                                                                            clone="CGX07-F03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 64.5%;
Matches 595; Conservative (
                                                                                                                                                                                                                 .1377
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ò

/sex="mixed male and female"

EST 28-APR-2004

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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Not1.oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies. a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                           1397 TGAACAATTACTCCCATTCCTAAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATATA 1456
                                                                                                                                                                                                                                                                                                                                                                                                                          1457 CATGGGACTCTCAAAGAATGCTAGATGACTCTGATTTGCTTAAGACCCTACCAACTACGG 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1576 AAGGGTTGTGATACACAGA---TGATTTATGACATGTTGCTAAGATTGAAATCCGTTCTC 1632
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Homo sapiens HELA CELLS COT 25.NORMALIZED"
/note="lgt gtrand cDNA was primed with a NotI-oligo(dT)
primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                             GAGCAGCTACAGCCAATCAGAACTACTTCCGCGCCTGCATGGATGACACCATTGCCTACA
                                                                                                                                                                                                                                                                                                                                                  863 TGAACTCTTTACACATCCCCGGACAGGTCCAGAACCGCATCAAGAACTGGTACGACTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 13, 2003 this sequence version replaced gi:30614460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DX401127 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo CDNA clone CSODK009YEl3 5-PRIME, mRNA sequence.

BX401127
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1 (bases 1 to 1054)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length CDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
/clone="CS0DK009YE13"
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KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                          /note="Vectors Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a CDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceeded by a synthetic Not1 site (first strand primer: 5.-CACTACTTCTACATCGCAGCGCCCCCC (175-3:). Following second strand synthesis, CDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the Not1 and EccRV sites of Express 1. Note that the EccRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxaTC' (where is ATC is the second half of the EccRV site, and xxx is desired from the cDNA sequence). A map of the Express 1 vector is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1037 ACAAAGCATATATCTACAGAGTTATTCGAACAACTGGATACTTGCTGTTTATTCTGCACA 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.openbiosystems.com/cdna_library_construction_fs
q.php#8 The primary library was transformed and amplified
in DH10B (Tl phage resistant) bacteria. Clones available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAAAGCATACATCTACAGGGGGATCAGGTCCACGTACCTGCTCTACTCTCTGCACA 562
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Pred. No. 8.9e-76;
0; Mismatches 402; Indels
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CGX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from Open Biosystems
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ilarity 61.5%;
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DQ032774 3444 bp DNA linear GSS 02-JUN-2005
Pan troglodytes CNGB1 gene, VIRTUAL TRANSCRIPT, partial sequenco,
                                                                                                                                                                                                                                                                         Hominidae, Pan.

1 (bases 1 to 344)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and Chimparzes
                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disease 1 to 3444)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.

Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,

White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sackton, T.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            737 CCGCAGACAACATACACTACTGGCTTATTGCGGACATCATATGTGATATCATCTACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           917 CAATAATACCATTTGATATTTGCTACCTCTTTTTGGGTTTAATCCAATGTTTAGAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        677 CTCTTGCCTATAACTGGAACTGCTGGTTTATACCACTGCGCCTCGTCTTCCCATATCAAA
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                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini
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al Similarity 35.8%; Score 333.8; DB 11; Length
al Similarity 35.8%; Pred. No. 1.9e-66;
A82; Conservative 0; Mismatches 865; Indels
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HC2747"
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                                                                                                                                                                                                           Pan troglodytes (chimpanzee)
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DQ032774.1 GI:66883983
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                                                                                Indels
                                        ; Score 363.8; DB 5;
; Pred. No. 1.5e-73;
35; Mismatches 353;
                                      Query Match
Best Local Similarity 60.8%;
Matches 611; Conservative 35
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                                                                                                       December 23, 2005, 17:07:01 ; Search time 446 Seconds (without alignments) 9684.921 Million cell updates/sec
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1: /cgn2 6/ptodata1/ina/1 COMB.seq:*

2: /cgn2 6/ptodata1/ina/5 COMB.seq:*

3: /cgn2 6/ptodata1/ina/6A COMB.seq:*

4: /cgn2 6/ptodata1/ina/6B COMB.seq:*

5: /cgn2 6/ptodata1/ina/H COMB.seq:*

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Sequence 14, Appl Sequence 18908, A Sequence 150501, Sequence 15059, A Sequence 2, Appl Sequence 2, Appl Sequence 11, Appl Sequence 1113, A Sequence 1113, A Sequence 139, Appl Sequence 189, Appl Sequence 189, Appl Sequence 159, Appl Sequence 175, Appl Sequence 175, Appl Sequence 175, Appl Sequence 175, Appl Sequence 175, Appl Sequence 175, Appl Sequence 175, Appl Sequence 175, Appl Sequence 175, Appl Sequence 175, Appl Sequence 175, Appl Sequence 175, Appl Sequence 1157, Appl Seque	SOCIATED DETECTION AND USES THEREOF	ength 2135; dels 15; Gaps	ATGCCGATGCCCAGCTACAC 399 	agaaaagttggtagagga 459 	CCACGGCTGTACCACCAGTA 519 	TGTTGTGGTTCAAAGTCAAA 579 	CAAACAGCATAGATTCATAC 639
2 US-08-232-463-14 3 US-09-949-016-38908 3 US-09-270-76-1505201 2 US-08-257-073-4 2 US-08-257-073-4 3 US-09-927-267-3 3 US-09-927-267-3 3 US-09-99-016-14581 3 US-09-949-016-14113 3 US-09-949-016-14113 3 US-09-949-016-14113 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919 3 US-09-949-016-38919	LIGNMENTS DIG IN KNOWN GENES ASS BEASE, METHODS OF 949,016 55 58 68 10n 4.0	.2%; Score 2049.4; DB 3; .2%; Pred. No. 0; e 0; Mismatches 1;	CACAAAACAAACGGCTGCAGCTCCTGTTATAAATGAGTATG 	acctggtgaaagaatgcgtcaagaacagcctctacaagaaaagttggtagagga 	ctctcacccgaagccagcccacaaactgcaaagco 	aaagaaagggatgataaggcaacagaacattactacaggctgttgtggttcaaagtcaaa 	aagatgcctttaacagagtacttaaagcgaattaaacttccaaacagcatagattcata(
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1720 GGCCCTGATGGTACTAAAGTTCTGGTTACTCTGAAAGCTGGGTCGGTGTTTGGAGAATC 177	0.00 TCTGAAAGGATCCTCATGAAGCCAGAGCGCAAGGCTAAGACCGCA		Qy 2260 CCTGAATGTACAGCAAGTCCTATTGCAGTGGAACCCCCACTCAGTTAGAACKGACA 119 Db 1906 CCTGAATGTACAGCAAGTCCTATTGCAGTGGAAGAACCCCACTCAGTTAGAACGACA 1966, Qy 2320 GTTTTACCCAGAGGGACTTCTCGTCAATCACTCATTATCAGCATGGCTCCTTCTGCTGAG 2179 Db 1966 GTTTTACCCAGAGGGACTTCTCGTCAATCACTCATTATCAGCATCGCTCCTTCTGCTGAG 2179 Cy 2380 GGCGGAGAAGAGGTTCTTACTATTGAATCAACTCATTATCAGCAATAA 2410 Db 2026 GGCGGAGAAGAGGTTCTTACTATTGAAGTCAAAGAAAAGCCTAAGCAATAA 2076	RESULT 2 US-09-949-016-5798 i Sequence 5798, Application US/09949016 j Partent No. 6812339 i GENERAL INFORMATION: TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TURRENT PELLING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-10-20 PRIOR PELLING DATE: 2000-09-08 PRIOR FILING DATE: 2000-09-08 PRIOR PELLING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SEQ ID NO 5798 LENGTH: 2139 TYPE: DNA TYPE: DNA TYPE: DNA CREANISM: Human
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; Sequence 17540, Application US/09949016
; Patent No. 6812339
; Patent No. 681239
; FARENRAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REPERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-3
; PRIOR FILING DATE: 2000-00-3
; PRIOR FILING DATE: 2000-00-3
; PRIOR FILING DATE: 2000-00-03
; PRIOR FILING DATE: 2000-00-08
                                                                         GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ITILE DE INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ICURENT APPLICATION NUMBER: US/09/949,016
CURRENT BILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAFESEQ for Windows Version 4.0
LENGTH: 99370
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13.6%; Score 330; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.3e-70;
Matches 330; Conservative 0; Mismatches 0;
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                                        Sequence 12816, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
RESULT 3
US-09-949-016-12816
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JAPELICATION VENTER, J. Craig et al.

APPLICATION VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 38930

LENGTH: 601
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                                                                                                                                                                          13.6%; Score 330; DB 3; Length 99
100.0%; Pred. No. 2.3e-70;
ive 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17540 LENGTH: 99370
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                                                                                                                                                                            Query Match 13.6
Best Local Similarity 100.
Matches 330; Conservative
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Matches 329; Conservative
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                                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17540
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ORGANISM: Human
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Sequence 205286, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPRENEUE: CLOOD 1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
SPIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
SPIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHAME: PRESECT FOR WINDOWS Version 4.0
SEQ ID NO 205286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 601;
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Matches 329; Conservative
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; Batent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PAPLICATION NUMBER: 60/237,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PELING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
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                            GATAAAGGAAGAGCCAGAAGAGAAGCCACTGGACAGACCTGAATGTACAGCAAGTCCT
                                                        294 GATAAAGGAAGAGCCCAGAAGAGAAGCCACTGGACGACCTGAATGTACAGCAAGTCCT
                                                                                                                          2281 ATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGACAGTTTTACCCCAGAGGGACTTCT
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Best Local Similarity 99.7
Matches 329; Conservative
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US-09-949-016-205286/c
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US-09-949-016-38931/c
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GENERAL INCORPATION:

GENERAL INCORPARATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRESESE for Windows Version 4.0

SEQ ID NO 205176

LEMCHT: 601
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| GENERAL INPORMATION:
| GENERAL INPORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF:
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF:
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF:
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/231,768
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: PRESEEQ for Windows Version 4.0
| SEQ ID NO 5678
| LENGTH: 2796
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100.0%; Pred. No. 8.2e-40;
tive 0; Mismatches 0;
                                                                                                                                                              RESULT 10
US-09-949-016-205176/c
Sequence 205176, Application US/09949016
; Patent No. 6812339
                              821 GACTCCAGTTTGTAAGAGGAGG 842
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Patent No. 6812339
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                                                               22 GACTCCAGTTTGTAAGAGGAGG
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Best Local Similarity 100.
Matches 202; Conservative
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US-09-949-016-205176
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US-09-949-016-5678
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| Sequence 38898/c
| Sequence 38898, Application US/09949016
| Sequence 38898, Application US/09949016
| Sequence 38898, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER. J Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| FILE REFERENCE: CL001307 |
| CURRENT FILLING DATE: 2000-04-14 |
| PRIOR FILLING DATE: 2000-10-03 |
| PRIOR FILLING DATE: 2000-10-03 |
| PRIOR FILLING DATE: 2000-10-03 |
| PRIOR FILLING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFFWARE: FREEDER for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                     CGTCAATCACTCATTATCAGCATGGCTCCTTCTGCTGAGGGCGGAGAAGAGGGTTCTTACT
                                                                                                                                                                                                                   2101 CAGAAGAAAGAAAATTCTGAAGGAGGAGGAAGAAGAAAGGAAAAGAAAATGAAGATAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 ATTGCAGTGCAGGAAGAACCCCACTCAGTTAGAAGGACAGTTTTACCCAGAGGGACTTCT
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                                                                                                         13.6%; Score 329.6; DB 3; Length 601; 99.7%; Pred. No. 3.3e-71;
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8.3%; Score 202; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 8.2e-40;
Matches 202; Conservative 0; Mismatches 0; Indels
                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2401 ATTGAAGTCAAAGAAAAGGCTAAGCAATAA 2430
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                                                                                                                                                           1; Mismatches
                                                                                                                                  Best Local Similarity 99.7
Matches 329; Conservative
                           ; ORGANISM: Human
US-09-949-016-205287
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Sequence 17420, Application US/09949016
; Sequence 17420, Application US/09949016
; Patent NO. 681239
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-00-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEO ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMAL OF THE TENTMA
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1002 TTATGTATATCGTCATTATCCACTGGAATGCATGTGTGTTTCTACTCTATTTCTAAAG 81061
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1854 GACGAGAGATGTACAAGGAAGGCAAACTCGCTGTGGTGGCGGAGATGATGAGGTCA 1913
                                                                                                                           CTAAAGTICTGGI----TACTCTGAAAGCTGGGTCGGTGTTTGGAGAAATC--AGCCTTC 1786
                                                                                                                                                                                                           1914 cicagringriciarrangacaridachacricadrangarchacarrictraacarra 1973
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                                                                                                                                                                                                                                                                                                                                                                              1974 AAGGGAGCAAAGCTGGCAATCGAAGAACGGCCAATATTAAAAGTATTGGCTACTCAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | NAME/KEY: misc_feature
| LCCATION: (1)...(84571)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17420
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                 CAGACAACATACACTACTGGCTTATTGCGGACATCATATGTGATATCATCTACCTTTATG
                                                                                                                                                                                         Score 181.2; DB 3; Length 2796;
                                                                                                                                                                                                                                                                             0; Mismatches 588;
                                                                                                                                                                                                                                     2.1e-34;
                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                     7.5%;
                                                                                                                                                                                                                                 Best Local Similarity 49.8
Matches 620; Conservative
                                                             , ORGANISM: Human
US-09-949-016-5678
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US-09-949-016-205175/c

i Sequence 205175, Application US/09949016

i Sequence 205175, Application US/09949016

i Sequence 205175, Application US/09949016

i Sequence 205175, Application US/09949016

i GENERAL INFORMATION:

i APPLICANT: VENTER, J Craig et al.

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i CURRENT APPLICATION NUMBER: US/09/949,016

i CURRENT FILING DATE: 2000-04-14

i PRIOR FILING DATE: 2000-10-03

i PRIOR PLILING DATE: 2000-10-03

i PRIOR APPLICATION NUMBER: 60/231,498

i PRIOR APPLICATION NUMBER: 60/231,498

i PRIOR APPLICATION NUMBER: 60/231,498

i PRIOR PLING DATE: 2000-09-08

i NUMBER OF SEQ ID NOS: 207012

i SOCTHARE: PSELSEQ for Windows Version 4.0

i ENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 601;
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llarity 99.3%; Pred. No. 2.3e-27;
Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 6.2%; Score 151.4; DB 3 al Similarity 99.3%; Pred. No. 2.3e-27; 152; Conservative 0; Mismatches 1
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.(6)
LENGTH: 601
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152; Conser
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US-09-949-016-205175
                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38897
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Best Local S:
Matches 152
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US-09-940-106-38897/c
| Sequence 38897, Application US/09949016
| Sequence 38897, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| FILE REPERENCE: CL001308
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                           11362 GAAATGTAAGCAAAGATATGGAAAAGAGGGTTATTAAATGGTTTGACTACCTGTGGACCA 81421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31482 AAATTGCCATCAACGTTCACTTAGACACATTAAAAAGGTACGCATTTTTGCTGATTGTG 81541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81422 ACAAAAAACAGTTGATGAGAAAGAAGTCTTAAAGTATCTACCTGATAAACTAAGAGCAG 81481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1880 TICTAGIGCATTATCCAGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGCTTTTAA 1939
                                                                                                                                                                                                                                                                  GTGGCCTTCCAGAACCACAAACTTTAATTTGAAATTGTTTTTCAACTCTTGAATTTTTTT 1285
                                                                                                                                                                                                                                                                                                                                                                                                1286 CTGGAGITITIGIGITCTCCAGITIAATTGGTCAGATGAGAGATGTGATTGGAGCAGCTA 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1346 CAGCCAATCAGAACTACTTCCGCGCCTGCATGGATGACACCATTGCCTACATGAACAATT 1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1646 ACTITIGICIGCAAAAAGGGAGAAAITIGGCAAGGAAAIGIAIAICAICAAGCAIGGAGAAG 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCAAGTTCTTGGAGGCCCTGATGGTACTAAAGTTCTGGT----TACTCTGAAAGCTGGG 1761
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                                                                                                                                    1166 GGGAAGGAAACGAGTATCTGAGATGTTATTATTGGGCAGTTCGAACTTTAATTACCATTG
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      1130 ATGAAGGAATTGGCACTACTAGATGGGTGTA
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RESULT

Search completed: December 23, 2005, 23:22:17 Job time : 451 secs

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Sequence

Sequence

Sequence 5, Appli Sequence 2, Appli Sequence 12975, Appli Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 19637, A Sequence 19637, A Sequence 19637, A Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli

Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

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y Sequence 3. Application US/0985828;
publication No. US2004013743341
| GENERAL INFORMATION:
| APPLICANT: Creech, Christopher D. APPLICANT: Jegla, Timothy J. TITLE OF INVENTION: GNG38: A Novel Cyclic Nucleotide-Gated Cation Channel;
| TITLE REFERENCE: 018512-006610US CURRENT FILING DATE: 2001-05-14
| PRIOR FILING DATE: 2000-05-15
| NUMBER OF SEQ ID NOS: 16
| SOFTWARE: Patentin Ver. 2.1
| LENGTH: 2430
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US-10-295-573-4
US-10-087-217-3
US-10-087-217-7
US-10-978-282-3
US-10-978-282-7
US-10-978-282-7
US-10-295-573-3
US-10-295-573-3
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US-11-097-143-26425
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US-10-189-507-1
US-10-114-153-17
US-10-029-677-23
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US-10-034-843-1
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100.0%; Score 2430;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches
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LOCATION: (1)..(2430)
OTHER INFORMATION: CNG3B
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ORGANISM: Homo sapiens
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Sequence 24368, A
Sequence 1, Appli
Sequence 27, Appl
                                                                                                                                                 December 23, 2005, 17:11:54; Search time 1732 Seconds (without alignments) 11601.956 Million cell updates/sec
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Sequence 2, Appli
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Sequence 16, Appl
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq: *

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10: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq: *
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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10 US-11-060-756-7105

6 US-10-189-507-3

6 US-10-189-507-3

6 US-10-189-507-3

6 US-10-189-507-198

10 US-10-450-763-1198

5 US-10-027-632-204539

10 US-11-037-143-26426

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US-09-925-065A-284516
US-11-097-143-24368
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Maximum Match 100%
Listing first 45 summaries
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Publication No. US2004013743341

SERENAL INFORMATION:

APPLICANT: Creech, Christopher D.

APPLICANT: Creech, Timothy J.

TITLE OF INVENTION: US00.00001000

FILE REFERENCE: 018512-00601008

CURRENT APPLICATION NUMBER: US/09/855,828

CURRENT APPLICATION NUMBER: US 60/204,445

FRIOR PILING DATE: 2001-05-14

FRIOR FILING DATE: 2000-05-15

NUMBER OF SEQ ID NOS: 16

SEQ ID NOS: 16

SEQ ID NOS: 16

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SEQ ID NOS: 16
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ATTGAAGTCAAAGAAAAGGCTAAGCAATAA 2430
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                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: (63)..(2492)
OTHER INFORMATION: CNG3B
                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                               LENGTH: 2703
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                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Complete CNG3B sequence derived from assembly
OTHER INFORMATION: PCR fragments
FEATURE:
NAME/RET: CDS
LOCATION: (112)..(2541)
OTHER INFORMATION: CNG3B
US-09-855-828-16
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Publication No. US2004013743341

GENERAL INFORMATION:
APPLICANT: Creech, Christopher D.
APPLICANT: Jegla, Timothy J.
APPLICANT: Jegla, Timothy J.
TILE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
FILE REFERENCE: 018512-00601003
CURRENT APPLICATION NUMBER: US/09/855,828
CURRENT APPLICATION NUMBER: US/09/855,828

CURRENT APPLICATION NUMBER: US/09/855,828

FRICK APPLICATION NUMBER: US/05-14

PRIOR FILING DATE: 2000-05-15

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 16
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                                                                                                                                     1803 CTGGTTACTCTGAAAGCTGGGTCGGTCGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGA
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                                                   GGAGGAGAAACCGTCGAACTGCCAATGTGGTGGCCCACGGGTTTGCCAATCTTTTAACT
                                                                                 CTAGACAAAAAGACCCTCCAAGAAATTCTAGTGCATTATCCAGATTCTGAAAGGATCCTC
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AAAGTTCTGGTTACTCTGAAAGCTGGGTCGTTTTGGAGAAATCAGCCTTCTAGCAGCA
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US-10-450-763-5457

Sequence 5457, Application US/10450763

PUBLICATION NO. US20050196754A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND FILE REFERENCE: 790CTP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR PILING DATE: 2001-03-30

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CUBTOM

SERVING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736
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             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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; NAME/KEY: SIMILAR; LOCATION: (1865); LOCATION: (1558)...(1865); OTHER INFORMATION: 86% homologous to Homo sapiens putative pls0,accession number; OTHER INFORMATION: U93563,Smith-Waterman Score=1961.
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APPLICANT: XU, HONG
APPLICANT: XI, HONG
APPLICANT: MYSER, BRYAN
APPLICANT: PRONIN, ALEXY
APPLICANT: ADLER, JON ELLIOT
APPLICANT: ADLER, JON ELLIOT
APPLICANT: ALLANARAS, NICHOLAS
TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
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                                                                                                            Length 2516
                                                                                                                                                  Indels
                                                                                                                DB 9;
                                                                                                              26.9%; Score 654.4; DB 9;
99.1%; Pred. No. 6.4e-131;
tive 0; Mismatches 6;
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                                                                                                                Query Match 26.9
Best Local Similarity 99.1
Matches 658; Conservative
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APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Ringner, Markus
APPLICANT: Ringner, Markus
APPLICANT: Peterseon, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
FILE REPERENCE: 11613.564511
CURRENT APPLICATION NUMBER: US/10/159,563
CURRENT FILING DATE: 2002-12-09
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 444
SOFTWARE: Patentin version 3.1
SEQ ID NO 147
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                                                  TGAACAATTACTCCATTCCTAAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATATA
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; Publication No. US20040009154A1
; GENERAL INFORMATION:
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Best Local Similarity 64.3
Matches 866; Conservative
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; TYPE: DNA
; ORGANISM: Homo
US-10-159-563-147
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TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
TITLE OF INVENTION: SMELL MODULATORS
FILE REFERENCE: 078003-0291857
CURRENT APPLICATION NUMBER: US/10/189,507
CURRENT APPLICATION NUMBER: 60/303,140
PRIOR PRIOR DATE: 2001-07-06
PRIOR PRIOR APPLICATION NUMBER: 60/303,140
PRIOR PLING DATE: 2001-07-06
PRIOR PLING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 12-
SOFTWARE: PATENTIN US: 2.1
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ORGANISM: Homo sapiens
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Matches 86
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LOCATION: (2009)..(3808)
OTHER INFORMATION: 99% homologous to Homo sapiens cyclic nucleotide-gated cation
OTHER INFORMATION: channel,accession number L15296,Smith-Waterman Score-3168.
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NAME/KEY: SIMILAR
LOCATION: (2009)...
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US-10-450-763-27462
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                                      APPLICATION THOSE OF TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REPERENCE: 790CH29/US CURRENT APPLICATION NUMBER: US/10/450,763 CURRENT FILING DATE: 2003-06-11 PRIOR FILING DATE: 2001-03-30 PRIOR PILING DATE: 2000-03-31 PRIOR PLILOR DATE: 2000-03-31 PRIOR PLILOR DATE: 2000-03-31 PRIOR PILING DATE: 2000-08-23 NUMBER OF SEQ ID NOS: 60736 SOFTWARE: CUSTOM SEQ ID NOS: 60736 SOFTWARE: CUSTOM SEQ ID NOS: 60736 SOFTWARE: CUSTOM SEQ ID NO 11960 SUSTAIN SEQ ID NO 11960 SUSTAIN SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND
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ORGANISM: Homo sapiens
Publication No. US20
GENERAL INFORMATION
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Best Local S:
Matches 536
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RESULT 10 US-10-450-763-11960 , Sequence 11960, Application US/10450763

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RESULT 12
US-10-027-632-204539
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                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (2115)..(1597)
OTHER INFORMATION: 99% homologous to Homo sapiens cone photoreceptor cyclic OTHER INFORMATION: nucleotide-gated channel beta subunit, accession number OTHER INFORMATION: AF272900, Smith-Waterman Score=917.
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21.3%; Score 518; DB 9; Length 2244;
Best Local Similarity 94.7%; Pred. No. 1.9e-101;
Matches 536; Conservative 0; Mismatches 30; Indels
                                                                APPLICATION THOUSE NOTE NUCLEIC ACIDS AND POLYPEPTIDES TILE REFERENCE: 790CH23/US CURRENT APPLICATION NUMBER: US/10/450,763 CURRENT FILING DATE: 2003-06-11 PRIOR PILING DATE: 2001-06-11 PRIOR PLING DATE: 2001-03-30 PRIOR PILING DATE: 2000-03-31 PRIOR PILING DATE: 2000-03-31 PRIOR PILING DATE: 2000-03-31 PRIOR PILING DATE: 2000-03-31 PRIOR PILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-08-23 VUMBER: CUSTOM NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23 VUMBER: CUSTOM NUMBER: 2244 LENGTH: 2244
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          Sequence 11988, Application US/10450763 Publication No. US20050196754A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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US-10-450-763-11988/c
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424 AAAGAAAATGAAGATAAACAAAAAGAAAATGAAGATAAAGGAAAAGAAAAGAAAAGAAAA 483
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                                                                                        APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR PLING DATE: 2000-07-20
PRIOR PLING DATE: 2000-07-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
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; Sequence 204539, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
Sequence 204539, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
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LOCATION: (1)...(680)
OTHER INFORMATION: n = A,T,C or G
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1307 GTTTAATTGGTCAGATGAGAGATGTGATTGGAGCAGCTACAGCCAATCAGAACTACTTCC 1366
      PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-2
PRIOR PILING DATE: 1999-11-2
PRIOR PILING DATE: 1999-11-2
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-2
PRIOR FILING DATE: 2000-01-2
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOUTHARRE: PRESERE PRESERE FRESERE FROM WINDER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SEQUENARE: PRESERE PRESERE FRESERE FROM WINDER: 60/191,637
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
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US-11-097-143-26426
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR PILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-02-29
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR PILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
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FRIOR FILING DATE: 1999-08-09
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GENDIGALION NO. US20050208558A1
GENDIGALION NO. US20050208558A1
GENDIGANT: Wenter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
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Pred. No. 8.2e-56;
0; Mismatches 0; Indels
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| LCCATION: (1)...(680)
| OTHER INFORMATION: n = A,T,C or G
US-10-027-632-204539
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Best Local Similarity 99.7%;
Matches 317; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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US-11-097-143-26426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 204539
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APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer', Laura
APPLICANT: Van 't Veer', Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
7 TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-115-999
CURRENT APPLICATION NUMBER: US/10/172,118
FRIOR APPLICATION NUMBER: 60/380,770
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
5 NUMBER OF SEQ ID NOS: 2699
5 SEQ ID NOS: 2699
6 CONTRACT OF SEQ ID NOS: 2699
7 TANAMUL DE APPLICATION NUMBER: 00/380,770
7 TANAMUL DE APPLICATION NUMBER: 00/380,770
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; DATABASE ACCESSION NUMBER: NM 000087
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-427
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Publication No. US20030224374A1
GENERAL INFORMATION:
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Mao, Mao
Roberts, Chris
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    Length 2500;
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Score 176.4; DB 6;
Pred. No. 1.6e-27;
0; Mismatches 591;
         7.3%;
         Query Match 7.3'
Best Local Similarity 49.6'
Matches 617; Conservative
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Db 1622 CTCAGTTTGTGGTATTGAGCAGCACCTTCGGTGAGATCATCTTAACATTA 1681

Qy 1787 TAGCAGCAGGAGACCGTGGAACTGGCGATGGTGGTGGCCACCGGTTTGCCATC 1846

1682 AAGGCACAAACTGCAATCGAAACAGCCCAATTTAAAAATTTAAAAATTTTAAATTTCAGAACTTTCAGAAAAAGACGCCAATATTAAAATTTTAACTCTAGAAAAAAGACCCTCCAAGAAATTCTAGTGCATTATCCAGATTCTGAAA 1906

Qy 1847 TTTTAACTCTAGAAAAAAGACCCTCCAAGAAATTCTAGTGCATTATCCAGATTCTGAAA 1906

Db 1742 TGTTCTGTCTCTCAAAAAGACCCTCATGAAAGCTCTAACTGAGTACCCAGATGCCAAAA 1801

Qy 1907 GGATCCTCATGAAAAAGCCAGAGTGCTTTTAAAGCAGAAGCT 1950

Db 1802 CTATGCTAGAAAAAGCAGAAGCAAATTTTAATGAAAAGGT 1845

Search completed: December 23, 2005, 23:51:25
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                                                                                                                                                                                  December 23, 2005, 17:34:16 ; Search time 312 Seconds (without alignments) 4041.860 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-995-561-2134

US-10-995-561-21194

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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: PMI GENOMICS, INC.
APPLICANT: PMI GENOMICS, INC.
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: FANTIN, Dennis
TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILION-2
CURRENT FALING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                      APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
FRIOR PELLING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALEATIN VETSION 3.1
SEQ ID NO 26195
LENGTH: 1603
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                                                                                                                                        Sequence 26195, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MI GENONICS, INC.
APPLICANT: BONISE, Sue K.
APPLICANT: KERK, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Bovine 19866880906828
US-10-750-185-26195
2416 AAGGCTAAGCAATAA 2430
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) NAME/KEY: misc feature
; LOCATION: (1)...(380749)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables : .
US-10-995-561-13216
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                                                                                                                                                                                                                           1318 CAGATGAGAGATGTGATTGGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCCTGCATG 1377
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 13116
                                                                                                                                                                                                                                                                      1626 CAGATGAGAGACGTAGGGGGCCCCCACCGCGGGAACAGACCTACTACTACCGCAGCTGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2148 TGAAGATAAACAAAAGAAAATGAAGATAAACAAAAAGAAAATGAAGATAAAGGAAAAGA
                                                                                                                                                                      Gaps
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3.0%; Score 72.2; DB 6; Length 380749;
Best Local Similarity 56.2%; Pred. No. 2.5e-05;
Matches 131; Conservative 2; Mismatches 100; Indels 0;
                                                                                                              Score 80.4; DB 6; Length 1687; Pred. No. 5.9e-08;
                                                                                                   3.3%; Score bv...
67.1%; Pred. No. 5.9e-08;
five 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 13216, Application US/10995561; Publication No. US20050272054A1; GENERAL INFORMATION:
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GENERAL INFORMATION: APPLICANT: WM1 GENOMICS, INC.
; TYPE: DNA
; ORGANISM: Bovine 19866881478981
US-10-750-185-47568
                                                                                                                                      Best Local Similarity 67.13
Matches 114; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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US-10-750-185-20334/c
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JS-11-121-086-88
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Best Local
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: MAI GENOMICS, INC.
APPLICANT: RESERVENCY CONT.
APPLICANT: ROSENFELD, David
APPLICANT: GOLM, Tom
APPLICANT: FAATIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE SEPRENCE MAIL100-2;
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
                                                                        APPLICANT: BATES, Camples
APPLICANT: BATES, Caphen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAIJ100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT PILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
SOFTWARE: PATENTE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTE: VERSION 3.1
SEQ ID NO 20334
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Pred. No. 4.1e-06;
0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Score 71.6; DB 6;
Pred. No. 2.9e-06;
0; Mismatches 29;
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US-10-750-185-26196
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SEQ ID NO 26196
LENGTH: 1442
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Best Local Similarity 75.4%;
Matches 89; Conservative
                 KERR, Richard
ROSENFELD, David
HOLM, Tom
                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Bovine MMBT06755
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DeNISE, Sue K.
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Best Local Similarity
Matches 89; Conserv
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ORGANISM:
                                                              APPLICANT
                                        APPLICANT
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RESULT 7

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2147 ATGAAGATAAACAAAAAGAAAATGAAGATAAACAAAAAGAAAATGAAGATAAAGGAAAAG 2206
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Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR SEQ ID NOS: 107
SOFTWARE: Patentin Version 3.3
SEQ ID NO 88
LENGTH: 184868
Sequence 84, Application US/11121086

Publication No. US2005026645941

GENERAL INFORMATION:

APPLICANT: POULSEN, TIM S.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REPERENCE: 09138.600.00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR PILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: Patentin version 3.3

SEQ ID NO 8: 107

SEQ ID NO 84

TYPE: DNA
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Best Local Similarity 57.3%; Pred. No. 0.0002;
Matches 121; Conservative 0; Mismatches 90; Indels
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Pred. No. 0.00058;
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US-11-121-086-84
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2096 CAGCTCAGAAGAAAGAAAATTCTGAAGGAGGAGGAAGAAGGAA-AAGAAAATGAAGAT 2154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21234, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT FILING DAFE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.7%; Score 64.4; DB 6; Length 191350; Best Local Similarity 64.4%; Pred. No. 0.00087; Matches 112; Conservative 0; Mismatches 61; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                          | FEATURE:
| NAME/KEY: misc feature
| LOCATION: (117565)..(117565)
| OTHER INFORMATION: n is a, c, g, or
| US-10-857-780-4
    or
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                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
NAME/KEY: (103359)...(103359)
OTHCRINFORMATION: n is a, c,
                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (95893) (95893)
OTHER INFORMATION: n is a, c,
                                                                                                                        NAME/KEY: misc feature
LOCATION: (81452)..(81452)
OTHER INFORMATION: n is a,
                                     NAME/KEY: misc feature
LOCATION: (64987)..(64987)
OTHER INFORMATION: n is a,
FEATURE:
OTHER INFORMATION: n is
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US-10-995-561-21234/c
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APPLICANT: ROTH, RICHARD B.
APPLICANT: ROTH, RICHARD B.
APPLICANT: RAWMERER, STEPAN M.
APPLICANT: REMELAND, RIKARD HENRY
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: HERHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
TITLE OF INVENTION: WHOMBER: US/10/857,780
FILE REFERENCE: SEQ-4069-CP
CURRENT FALING DATE: 2004-05-28
PRIOR FILING DATE: 2003-11-25
PRIOR PELING DATE: 2003-07-24
PRIOR PELING DATE: 2003-07-24
PRIOR FILING DATE: 2003-07-24
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE PATENTING VERSION 3.2
                                                         55672 AAAGAAAAAGAAACTCAGTGAGTTACAGAAAACACAAATCCACAGAGGG 55721
                                                                                                       2244 GAAGCCACTGGACAGACCTGAATGTACAGCAAGTCCTATTGCAGTGGAGG 2293
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LOCATION: (61207)..(61207)
OTHER INFORMATION: n is a, c,
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LOCATION: (26334)..(26334)
OTHER INFORMATION: n is a,
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NAME/KEY: misc feature
LOCATION: (57355)..(57355)
OTHER INFORMATION: n is a,
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LOCATION: (16914)..(16914)
OTHER INFORMATION: n is a,
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LOCATION: (19266)..(19266)
OTHER INFORMATION: n is a,
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LOCATION: (34467)..(34472)
OTHER INFORMATION: n is a,
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LOCATION: (38627)..(38628)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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LENGTH: 191350
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SEQ ID NO 21195
LENGTH: 201
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Publication No US20050272054A1
GERREAL INFORMATION:
GENETAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO01559
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 87702
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21194
2040 AGGAGGCACAGGAAAAGCAAGTCTTGCAAGACTACTCAAATTGAAGCGAGGAAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/11121086
Publication No. US2005026645941
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION:
TITLE OF INVERTION:
TITLE OF INVERTION NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOSTWARE: PATENTIN version 3.3
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ORGANISM: Homo sapiens
US-10-995-561-21194
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US-11-121-086-25
                                                2250 ACTGGA 2255
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US-11-121-086-25
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL,
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION:
PILE REFERENCE: CLO01559
                                                                                                                                                                       2130 GGAAGAAGGAAAAGAAAATGAAGATAAACAAAAAGAAAATGAAGATAAACAAAAAAGAAAA 2189
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION:
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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58.6%; Pred. No. 0.00014;
tive 0; Mismatches 77; Indel8
Length 201
                                            77; Indels
Score 62.8; DB 6;
Pred. No. 0.00014;
0; Mismatches 77;
    2.6%;
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Matches 109, Conservative
  Query Match
Best Local Similarity 58.65
Matches 109; Conservative
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US-10-995-561-21195
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US-10-995-561-21351/c
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CENERAL INFORMATION: US20050272054A1
GENERAL INFORMATION: US20050272054A1
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995, 561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PRESECTE OF WINDOWS VERSION 4.0
SEQ ID NO 13220
LENGTH: 28037
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                                                                                                                                                                                           Length 201;
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                                                                                                                                                                                         Score 62.8; DB 6;
Pred. No. 0.00014;
0; Mismatches 72;
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CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ TO NO 21351
LENGTH: 201
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Best Local Similarity 59.61
Matches 106; Conservative
                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-21351
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; ORGANISM: Homo sapiens
US-10-995-561-13220
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US-10-995-561-13220/c
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AF272900 Homo sapi
AF28520 Homo sapi
AF490511 Canis fam
AJ343572 Mus muscu
CQ716885 Sequence
L15297 Homo sapien
L15296 Homo sapien
CQ715590 Sequence
BC044198 Homo sapi
CQ715550 Sequence
BC04514 Mus muscu
AF074012 Bos tauru
AF074013 Bos tauru
X894707 B.taurus mR
AF074014 Bos tauru
X89656 B.taurus mR
AJ000496 Ratus no
CQ880122 Sequence
                                                           December 23, 2005, 16:49:01 ; Search time 11791 Seconds (without alignments) 11714.832 Million cell updates/sec
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1 atgtttaaatcgctgacaaa......aagaaaaggctaagcaataa 2430
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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CQ715550
BC045114
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AF074014
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Match Length DB
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Rattus		AC013751 Homo sapi	ខ	ထ	σ	BC046523 Mus muscu		\sim	U85404 Sus scrofa	~			U83905 Canis famil	AX930698 Sequence	M84741 Human cGMP-	taur.	AFS47222 Homo sapi	Homo	Pan	74 Pan	U19717 Mus musculu	M84742 Mus musculu	AF091302 Limulus p	AC161933 Bos tauru	AC154999 Bos tauru	AL772281 Mouse DNA	
RNCNG43	AF068572	AC013751	CEU73476	CQ598668	BT001439	BC046523	AF015728	AY060725	SSU85404	CQ716337	S42457	CFACGMP	CFU83905	AX930698	HUMCGMP	BTCGMPCH	AF547222	AC107068	AC161820	AC164974	MMU19717	MUSCNCG	AF091302	AC161933	AC154999	AL772281	
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568	568	330	237.4	223	223	217.8	96	187.4	181.2	181.2	181.2	176.8	176.8	176.4	176.4	173.6	169.8	169.8	166.6	166.6	166.4	164.8	162.4	162.2	10	161.4	
19	20	21	22	23	24	25	56	27	28	5	9	31	32	6	4	35	36	37	38	39	40	41	42	43	44	45	
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ALIGNMENTS

	AF272900 AF2720		Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Euarchontoglires; Primates; Catarrhini;		Kellner, U., Spegal, R., Anastasi, M., Zrenner, E., Sharpe, L.T. and	Wissinger, B.	Mutations in the CNGB3 gene encoding the beta-subunit of the cone	photoreceptor cGMP-gated channel are responsible for achromatopsia		2					Laboratory, Aur der Morgenstelle 15, Tuebingen D-72076, Germany			/mol type="mRNA"	/db xref="taxon:9606"	1		472476	/gene="CNGB3"	/codon_start=1	/product="cone photoreceptor cyclic nucleotide-gated	channel beta Bubunit"	/protein_id="AAF86274.1"	/dh *ref="GT・9047066"
RESULT 1 AF272900	LOCUS	ACCESSION VERSION	KEYWORDS SOURCE	ORGANISM		REFERENCE	AUTHORS		TITLE		JOURNAL	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL		FEATURES	21000			dene	1	CDS						

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RLVFPYQTADNIHYWLIADIICDIIYLYDWLFIQPRLOFRAGDIIVOSNELRKHYRT
STKFQLDVAS.IIPPDICYLEFGRNPWRFANRWLKYTSFEFNHHLESIMDKAYIYRY
STKFQLDVASIIPPDICYLEFGRNPWRFANRWLYTSFFFNHHLESIMDKAYIYRVI
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BPQTLFEILYFQLLNFFSGVFVFSSLIGGMRDVIGAATANQNYFRACMDDTIAYMNYS
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AKTARTPPRKTANVAHGFANLLTLDKKTLLGGTGKASLARLKHKREQAAQKKENSE
GGBEBGKENBDKQKENBERGKENBERGKGREDEEKPLLKHKREQAAQKKENSE
GGBEBGKENBDKQKENBERGKENBERCHGRENBERCTASPIAVEE
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/product="cone photoreceptor cGMP-gated cation channel
beta-subunit"
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84.3%; Score 2049.4;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2075; Conservative 0; Mismatches
                                                                               'note="membrane channel;
                                                                                                                                          /protein_id="AAF80179.1"
/db_xref="GI:8843948"
                                           244. .2076
/gene="CNGB3"
                             'gene="CNGB3"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Submitted (25-JAN-2000) Opthalmology, Johns Hopkins School
Medicine, 600 North Wolfe Street, Baltimore, MD 21287, USA
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Sundin,O.H., Yang,J.-M., Li,Y., Zhu,D., Silva,E.D. and
Maumenee,I.H.
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1 (bases 1 to 2135)
Sundin,O.H., Yang,J.M., Li,Y., Zhu,D.,
Sllva,E.D. and Mumenee,I.H.
Genetic basis of total colourblindness
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/organism="Homo sapiens"
/nol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="8"
/map="8q21-q22"
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AF228520.1 GI:8843947
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1726 TTGAAGCGAGGCAAGCAGCTCAGAAGA	RESULT 3 AF490511 LOCUS CAN18 familiaris cyclic nucleot (CNOB3) mRNA, complete cds. AF490511.1 G1:22023792 KEYWORDS CAN18 familiaris (dog) CAN18 CAN18 familiaris (dog) CAN19 FEATHORS CAN18 CAN19 FEATHORS; CAN19 CAN19 CAN19 CAN19 REFERENCE 1 (bases 1 to 2826) AUTHORS Sidjanin, D.J., Lowe, J.K., McElw Sargan, D.R., Aguirre, G.D., ACLI TITLE CAN10 CAN28 mutations establis to the human achromatopsis locu JOURNAL Hum. MOI. Genet. 11 (16), 1823- TITLE Sidjanin, D.J., Lowe, J.K., McElw Sargan, D.R., Aguirre, G.D., ACLI JOURNAL Hum. MOI. Genet. 11 (16), 1823- AUTHORS Sidjanin, D.J., Lowe, J.K., McElw Sargan, D.R., Aguirre, G.D., ACLI JOURNAL Burect Submission JOURNAL Burect Submission JOURNAL COMPACTOR Hill Rd., Ithaca, NY FEATURES CDS (ACCALION/Qualifiers CDS (ACCALION/Qualifiers CDS (ACCALION/Qualifiers CDS (ACCALION/Qualifiers CDS (ACCALION/Qualifiers CDS (ACCALION/Qualifiers CDS (ACCALION/Qualifiers CDS (ACCALION/Qualifiers CDS (ACCALION/Qualifiers CDS (ACCALION/Qualifiers CDS (ACCALION/QUALIFIER) CON ARMARIALITICGLERPYTHOUL HUMSNELKRHYRSSTRFOLD DIMVOSNELKRHYRSSTRFOLD HUMSNELKRHYRSSTRFOLD HUMSNELKRHYRSSTRFOLD HUMSNELKRHYRSSTRFOLD HUMSNELKRHYRSTRFOLD CON STATE IN TAYMNOCHLIPELYPYCOLORI CON STATE IN TAYMNOCHLIPELYPYCOLORI CON STATE IN TAYMNOCHLIPELYPYCOLORI CON STATE IN TAYMNOCHLIPELYPYCOLORI CON STATE IN TAYMNOCHLIPELYPYCOLORI CON STATE IN TAYMNOCHLIPELYPYCOLORI CON STATE IN TAYMNOCHLIPELYPYCOLORI CON STATE IN TAYMNOCHLIPELYPYCOLORI CON STATE IN TAYMNOCHLIPELYPYCOLORI CON STATE IN TAYMNOCHLIPELYPYCOLORI CON STATE ACCALION/QUALIFICENT TAYMNOCHLIPELYPYCOLORI CON STATE ACCALION/QUALIFICENT TAYMNOCHLIPELYPYCOLORI CON STATE ACCALION/QUALIFICENT TAYMNOCHLIPELYPYCOLORI CON STATE ACCALION/QUALIFICENT TAYMNOCHLIPELYPYCOLORI CON STATE ACCALION/QUALIFICENT TAYMNOCHLIPELYPYCOLORI CON STATE ACCALION/QUALIFICENT TAYMNOCHLIPELYPYCOLORI CON STATE ACCALION/QUALIFICENT TAYMNOCHLIPELYPYCOLORI CON STATE ACCALION/QUALIFICENT TAYMNOCHLIPELYPYCOLORI CON STATE ACCALION/QUALIFICENT TAYMNOCHLIPELYPYCOLORI CON STATE ACCALION/QUALIFICENT TAY
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MQDKI SEKNSLRDLTTNPNHOHPTESKGAMSEOKEMETGK
KYADAOLINIUVRRINGPTHLYKKKLAEGDI SS PEASPOTAK
KYYHILCFKFOKMPLTEYLKRFRLEGSI DS YTDRIVYLMLL
FPYOTPDNTHYWFI TDI TCDI I YLCDMLLI OPPLOFI KGG
FRQLDASWMPPDDYFYLFGFNDV FRWNYTSFFFFNH
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TYSFEI VFOLLNFFSOV FVFSEL I GOMODVI GAATANONNF
NYQNNYTHYFRUDSORMDESDLECTTLP VMOLALTVU
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otide gated channel beta subunit
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heria; Carnivora; Fissipedia; Canidae;
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land,G.M. and Ostrander,E.A.
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cus ACHM3
3-1833 (2002)
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land,G.M. and Ostrander,E.A.
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	1164 GGTGTATAACGGTGAAGGAACAAGTATCTAAGATGTTATTTGGCCTGTTCGAACTTT 1 1215 AATTACCATTGGTGCCTTCCAGAACCACAAACTTTATTTGAAATTGTTTTAACCTTTTAACATTGAGGGCCTTTT 1 1224 AATTACCATTGGGGCCTTCCAGAACCACAAACTTTATTTGAAATTGTTTTTCAACTCTT 1 1224 AATTACCATTGGGGCCTTCCAGAACCACAAACAAACATCATTTGAAATTGTTTTTCAACTGTT 1	1275 GAATTTTTTTTGGAGTTTTTGGTTCTCCAGTTTAATTGGTCAGATGAGAGTGTGAT 1	1344 TGGGGGCGCCCATCAGAACAACTTCCGAATCAGGATCATCGATCATTCCTA 1 1395 CATGAACAATAACTTCCTAAACTTGTGCAAAGGGGGGTTCGGATCATTGGTATGATA 1 1194 CATGAACATTACTCCAAAGAACTGGGAAAGGGGGTTCGGATCATGTATGATA 1 1104 CATGAACACTTATTCCATTCCTAAGAATGTGCAGAATGGGGTTCGGACTTGGTATGAATA 1	1455 TACATGGGACTCTCAAAGAATGCTAGATGAGTCTGATTTGCTTAAGACCCTACCAACTAC 1	1515 GGTCCAGTTAGCCCTCGCCATTGATGTGAACTTCAGCATCAGCAAAGTCGACTTGTT 1	1584 CAAGGGTTGTGATACACAGATGATTTATGACATGCTGCTAAGATTCCACTGTTA 1 1635 TTTGCCTGGTGACTTTGTCTGCAAAAAAGGGGAGAAATTGGCAAAATTGCCTGGTAATATCATATA 1 1644 TTTGCCTGGTGACTTTGTCTGCAAAAAAAATGGCAAGGAAATATCATATATCATA 1		ro 4	ru 4	1875 AGAATTCTAGTGCATTATCCAGATTCTGAAGGATCCTCATGAAGAAAGCCAGAGTGCT 1 	1935 TTTAAAGCAGAAGGCTAAGACCGCAGAAGCACCCCCCAAGAAAGA	1995 CTTCCCACGAAAGAAGACACCCAAACTGTTTAAAACTCTCCTAGGAGGCACAGGAAA 2	2055 AGCAAGTCTTGCAAGACTACTCAAATTGAAGCGAGCAAGCA
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HYPDSEKLLMKKASVLLKKKAPATETTPPRKGLAFLPPPKQETPKIFKALLGGT LTRLLKLKREQTIQKTSENSEGGGKRREYEDKEREPSEKILDSSECRANCIIA QSIRRAALPRGTTRQSLIISMAPSAEAGEEVLTIEVKEKAKQ" SOSTE 1682.2; DB 4; Length 2826; Local Similarity 83.6%; Pred. No. 2.4e-286; hee 1972; Conservative 0; Mismatches 312; Indels 75; Gaps	GAATGAAGGCTCTCACCCAAGTAATCAGTCTCAGCAAACCACAGGACACAGGAAGAAA [11]	4 CAAAAGTGAAAATAAATCTCTCCAAACCAAGATGACTCCAGTCAGGTTTGAAGAATCACA 8 CACCAACATACAAGACAAACTCTCCAAGAAAAATTCCTCTGGAGATCTGACCACAAACCC	TGCCTCAAATGCAGCAGAACCACTTGGAGTGCCAGAGAGAAGGAGTCC 3	324 TGGGAAAGAGCCTAGTCAGCCCAAAAAGCAAACCCCTTGGAGTCCCTGTTATAAATGA 383 378 GTATGCCGATGCCCACCTACACAACCTGGTGAAAAGAATGCGTCAAAGAACAGCCTCTA 437 184 GTATGCTGATGCTACACTACACAACCTGGTGAAAAGAATGCGTCAAAGAACAATGCTCTA 443	CAAGAAAAGTTGGTAGAGGAGATCTCTCCTCACCCGAAGCCAGCC	498 GCCCACGGCTGTACCACCAGTAAAAGCGATGATAAGCCAACAGAACATTACTA 554		TTCCCATATCA 7	AACCGCAGACAACAACAACAACAACAACAACAACAAAAAA	795 TIATGATATGCTATTTATCCAGCCCAGACTCCAGTTTGTAAGAGGAGGACATAATAGT 854	GGATTCAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAATTCAGTTGGATGTCGC 9	ATCAATAATACCATTTGATATTTGCTACCTCTTTTGGGTTTAATCCAATGTTTAGAGC	924 GICAGIAANGCCAITIGANGTITITIACCICITICITICAGITIAANCCAGIATITAAGAN 983 975 AAATAGGATGTTAAAGTACACTTCATTTTTGAATTTAATCATCCAGGGTCTATAAT 1034
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Matches 1795; Conservative (
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AJ243572
AJ243572.1 GI:6851039
CNG6 gene; cyclic nucleotide-gated channel subunit CNG6 MJ243572.1 MJ8 musculus (house mouse)
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protein id="CAB71152.1"
db_xref="G1:6851040"
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                                                                                                                                                    2292 GGAAGAACCCCACTCAGTTAGAAGGACAGTTTTACCCCAGAGGGACTTCTCGTCAATCACT
                                                                                                                                                                      Submitted (26-JUL-1999) Gerstner A., Technische Universitaet
Muenchen, Pharmakologie und Toxikologie, Biedersteiner Str. 29,
D-80802 Muenchen, GERMANY
Location/Qualifiers
                                         AGAGCCAGAAGAGAGCCACTGGACAGACCTGAATGTACAGCAAGTCCTATTGCAGTGGA
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Molecular cloning and functional characterization of a new
modulatory cyclic nucleotide-gated channel subunit from mouse
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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nucleotide-gated cation channel"
                  AAACTCTGAAGAAGGAGGGGTAAAAGAAGAGAATATG-
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/db_xref="InterPro:IPR000595"
/db_xref="InterPro:IPR001622"
/db_xref="InterPro:IPR005821"
/db_xref="MGI:1353562"
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/strain="c57Black6"
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TAYNWICKLLPVRLVFPCQTPDNKNYWITTOTVCDITYLCDILLIOPRLQFRGGEII
SUNDSBLKKRYKRSSTKERMDVASLLPFBLVITFGTWPIFALRILKTTSFFEFNHHLE
SIMDKAYVTRVIRTTGYLLELLHINACVYWASDYEGIGSTKWYNGEGNKYLRCFYW
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MDHIIAYMNKYSIPQSVQYRVRTWLEYTWNSQRILDESNLLENLFTAMQLSIALDINF
SIDKVELEKGCDTQMIYDLLALKASTIYLEGFFCKRMYITHGENLFTAMQLSIALDINF
SIGKVLLYKAGSYFGEISLLAKGGGNRRTADVVAHGFANLLTLDKKTLOGILLHYP
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TNISPKQENNSKLKEHQDTFSFKFORVPVKEHLRRMILPRSIDSYTDRVYLLMILLIVT
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7; 137 316 259 117 97.1 111 202 197 257 4 56 4 3.7 496 464 556 5,54 616 614 673 674 733 734 793 794 260 CAGCAA---AGAAGACAACAGCACTGGGGAAAACTCTCTCAGAGTTTCACCCCAAATCC GAATGAAGAAGCTCTCACCCAAGTAATCAGTCTCAGCAAACCACAGCACAGGAAGAAA GAAGAAACTCTGCCCCCAACCTGAGCAGTCTTTCTCAGCCAACCATAGCACAGGAGAAAAA ccadacticadadadecrerengageageageaca - - cedareacarricadadereaca 437 AIATACTGATGCCCACCTACACAACCTAGTGGAAAGAATGCGTGAAAGGACTGCTCTCTA CA---CGTTTTCTTTCAAACCCCAGAGAGTCCCAGTAAAAGAGCACCTACGAAGAATGAT CAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTCACGTCTGAAGAGCCACA CACCAACATACAAGACAAACTCTCCAAGAAAATTCCTCTGGAGATCTGGACCACAAACCC TGACCCTCAAAATGCAGCAGAACCAAACTGGAACAGTGCCAGAGCAGAAATGGACCC TGACCCTGAATGTCGAGGGAACTCACCAGAACAATGGCAGAGATGGAGAAAACTAGGAC CGGGAAAGAAGGTCCAAAACAGCCCACAAAACAAAACCGCCTGCAGCTCCTGTTTATAAATGA 377 reseahasahasaccastrascrittahasakcahastrestrahahastrahaharah GTATGCCGATGCCCAGCTACACACCTGGTGAAAAAAATGCGTCAAAGAACAGCCCTCTA CAAGAAAAAGTTGGTAGAGGGAG---ATCTCTCCTCACCCGAAGCCAGCCCACAACTGC AAAGCCCACGGCTGTACCACCAGTAAAAGAAAGCGATGATAAGCCAACAGAACATTACTA CAGGCTGTTGTGGGTTCAAAGTCAAAAGATGCCTTTAACAGAGTACTTAAAGCGAATTAA **ACTTCCAAACAGCATAGATTCATACACAGATCGACTCTATCTCCTGTGGCTCTTGTTGT** 674 Actroccagaagcaragacrocracacagarcgggrotarcrorrergggcrocraca CACTCTTGCCTATAACTGGAACTGCTGGTTTATACCACTGCGCCTCGTCTTCCCATATCA 734 caccarridegraraacridaaacrigridecrideraceaacredecrecerecea **AACCGCAGACACATACACTACTGGCTTATTGCGGACATCATATGTGATATCATCTAACCT** Gaps 65; Length 4710; Score 1362.4; DB 9; Length Pred. No. 4.2e-230; 0; Mismatches 496; Indels

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Momo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other
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                               CTTCCCACCGAAAGAAGAGACACCCAAACTGTTTAAAACTCTCCTAGGAGGCACAGGAAA
                                               2054 TITCCCACCAAAAGAAGACACCCCCAAIGCTTAAAGTTCTCCTAGGAAACACACAGGAAA
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PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 2819 from Patent WO02068579.
CQ716885. GI:42277742
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                                                                   GGACAAAGCATATATCTACAGAGTTATTCGAACAACTGGATACTTGCTGTTTATTCTGCA 1094
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                                                                                                                AAATAGGATGTTAAAGTACACTTCATTTTTTGAATTTAATCATCACCTAGAGTCTATAAT 1034
                    973
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                                                                                                                                 1214 GGTCTATAATGGTGAAGGCAACAAGTATCTGCGATGCTTTTATTGGGCAGTTCGAACTTT
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 ATCAATAATACCATTTGATATTTGCTACCTCTTCTTTGGGTTTAATCCAATGTTTAGAGC
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FQGCDRQMI FDMLKRLRSVVYLPNDYVCKKGEIGREMY I IQAGOVQVLGGPDGKSVLV
TLKAGSVFGEISLLAVGGGNRRTANVVAHGFTNLF I LDKKDLNEI LVHY PESQKLLRK
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2 (bases 1 to 3025)
Ahamed, BA.
Direct Submission
Submitted (17-MAY-1993) Basheer Ahamed, Biomedical Engineering, Johns Hopkins School of Medicine, Baltimore, MD 21205, USA Original source text: Homo sapiens DNA.
Location/Qualifiers
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                                                                                                                                                                                                                /organism="Homo sapiens"
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389. .2460
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                      GATCTGACCACAAACCCTGACCCTCAAAATGCAGCAGAACCAACTGGAACAGTGCCAGAG
                                                                                                                                                                                                                                                                                                                                                      361 GCTCCTGTTATAAATGAGTATGCCGATGCCCAGCTACACAACCAGGTGAAAAGAATGCGT
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truce 362 (6422), 764-767 (1993)
7682292
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1 (bases 1 to 3025)
Chen, T.Y., Peng, Y.W., Dhallan, R.S., Ahamed, B., Reed, R.R.
Yau, K.W.
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                                                                       Ahamed, Ba. Abanes 1 to 3408)
Ahamed, Ba. Basheer Ahamed, Biomedical Engineering, Johns Hopkins School of Medicine, Baltimore, MD 21205, USA Original Bource text: Homo sapiens DNA.

Location/Qualifiers
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64.3%; Pred. No. 7.8e-92;
iive 0; Mismatches 481;
Nature 362 (6422), 764-767 (1993)
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1 (bases 1 to 3408)
Chen, T. Y., Peng, Y. W., Dhallan, R. S., Ahamed, B., Reed, R. R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAATGTGGTGGCCCACGGGTTTGCCAATCTTTAACTCTAGACAAAAAGACCCTCCAAG
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                                                                                                                          ATTTTTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAATTGGTCAGATGAGATGTGATTG
                                                                                                                                                                                                                                                                                                                                                                                        GAGCAGCTACAGCCAATCAGAACTACTTCCGCGCCTGCATGGATGACACCATTGCCTACA
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Cyclic nucleotide-gated cation channel; retinal protein.
Homo sapiens (human)
Homo sapiens
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/evidence=experimental
/product="cGNP-gated cation channel beta subunit"
/protein_id="AAB63197.1"
/db_xref="G1:1518639"
/translation="MLGWVQRVLPQPPGTPRKTKMQEEEEVEPEPEMBAEVEPEPNPE
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THWAMKQUSEKUIPQPPHSITEDBAQILGGSTGOTGTDEPNRALEADOTRPGILELU
WLEQNLERVLAQPPRSSEWRDEPAVATGASDPAPPGRPOGMGPKLQARETSSI.PTP
IPLQPKEEPKEAPAPEPQPGSQAQTSSLPPTRDPARLVAWVLHRLEMALPQPVIHGKT
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BENKAVEWRPRELSRIBERSEBEEBEEBEEBETVELLDSCVVSQVGVGVGSE
DGTRPQSTSDQKLWERSDBEKREBEEBETBETVELDSCVVSQVGVGVGSE
DGTRPQSTSDQKLWEFVGERAKKEABEKAREBEREKEPOWAFTKEFPGAF
ABAASGVPATKQHPEVQVEDTDADSCPLMAEENPPSTVLPPPSPGMAFTKEFPGAF
RTRKALPSEDDEABELKALSPAESPVAMSPPTTFKOTDGORAASTVASTVASIIND
RLQELVKLFYERTTRYKVEKLIDPDVTSDESSPKPSPAKKAPEPPAPERPVEEF
HYCDMLCCKFKHRPWKKYQFPQSIDPLTNLMYVLWLFFVVMAMWNCWLIPVRWAFPY
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DLLSLLPLDFLYLKVGVNPLLRLPRCLKYMAFFEFNSRLESILSKAYVYRVIRTTAYL
LYSLHLNSCLYYWASAYQGLGSTHWVYDGVGNSYIRCYYFAVKTLITIGGLPDPKTLF
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NRKKWYBYETWASQMLDESELMVQLPDKMRLDLAIDVNY NI YSKVALFOGCDRQNI F
DMLKRLRSVYYLPNDYCKKGEI GREMY I I OAGQVVQLGGPDGKSVLYTLAGSVPGE
I SLLAVGGGNRRTANVVAHGFTNLFI LDKKDLNEI LVHY PESOKLLRKKARRRINGSN
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KHEELVEQAKSSQDVKGEEGSAAPDOHTHPKEAATDPPAPRTPPEPPGSPPSSPPPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-MAY-1996) Pittler S. J., Department of Biochemistry and Molecular Bacology, University of South Alabama College of Medicine, 307 University Blvd, Mobile, AL 36688-0002, USA Location/Qualifiers
                            Hominidae, Homo.

I (bases 1 to 330)

Ardell, M.D., Makhija, A.K., Oliveira, L., Miniou, P.,
Viegas-Pequignot, E. and Pittler, S.J.

Viegas-Pequignot, E. and Chromosomal localization of human GAR1
(CNCG3L), a homolog of the third subunit of bovine photoreceptor
GMP-gated channel
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The beta subunit of human rod photoreceptor cGMP-gated cation channel is generated from a complex transcription unit
PEBS Lett. 389 (2), 213-218 (1996)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/tissue_type="retina"
/dev_stage="adult"
1. .4033
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="16"
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/gene="CNCG2"
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gene="CNCG2"
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Pittler, S.J.
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Human cGMP-gated cation channel beta subunit (CNCG2) mRNA, complete
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1. (bases 1 to 4382)

1. (convald, M.E., Yu, W.P., Yu, H.H. and Yau, K.W.

1. (convald, M.E., Yu, W.P., Yu, H.H. and Yau, K.W.

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2. (bases 1 to 4382)

3. (convald, M.E., Yu, W.P., Yu, H.H. and Yau, K.W.

Direct Submission

3. (convald, M.E., Yu, W.P., Yu, H.H. and Yau, K.W.

Direct Submission

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                        2948 AGGGCTGTGACCGGCAGATGATCTTTGACATGCTGAAGAGGCTTCGCTCTTGTCTACC
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Altachul, S.P., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altachul, S.P., Zeeberg, B., Buecow, K.H., Schaefer, C.F., Bhac, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheerz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Holton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J. W., Green, E.D.,
Bickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
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Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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TGCCTGGTGACTTTGTCTGCAAAAAGGGAGAAATTGGCAAGGAAATGTATATCATCAAGC
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
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                                                                                                                                                    Length 4320;
                                                                                                                                                                                                                      Indels
                                                                                                                                             Score 575.8; DB 6;
Pred. No. 1.4e-91;
                                                                                                                                                                                                                      482;
                                                                                                                                                                                                                      0; Mismatches
              /mol_type="unassigned
/db_xref="taxon:9606"
                                                                                                                                                 23.7%;
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                         Similarity
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Matches 865;
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                                                                                                      Gaithereburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcahgai.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Houffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Houffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karline,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
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BEKEERKEEERKEEEVKKEEGEATNSTVPATKEHPELQVEDTDADSGPLIPEETL
PPPERPPPSEVKSDTLVYPGAAAAGHRKKLPSQDDABELELASIOBELBEVANANDPTT
PQGAAGQDRAASTASONSAIINDLOGILYWRERETTEKVKEKLIDPDVTSDESPKP
PAKKAPEPDPAQKPAASTASONSAIINDLOGILYWRERETTEKVKEKLIDPDVTSDESPKP
PAKKAPEPDPAQKPAASTASONSAIINDLOGILYWRERETTEKVKEKLIDPDVTSDESPKP
PAKKAPEPDPAQKPAASTASONSAINTALLOGILLMDDYLCDFIYLLDITUPQWRLQFVK
GGDIITDKKAMRNNCWLIPWRAPPYQRADNIHFWLLMDYLCDFIYLLDITUPQWRLQFVK
GGDIITDKKAMRNNYLKSRRFMDLLLYSLHINSCLYYWASAFQGIGTHVYDGVGNSYI
RCYYWAVKTIITIGGLPDPQTLFEIVFQLHUNSCLYYWASAFQGIGTHWYDGVGNSYI
YYSCWDSTVKXWNFYKIPRSVQNRVKTWYEYTWHSQGMLDESELMVQLPDRGNRLDLA
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QVLGGPDGKAVLVTLKAGSVFGEISLLAVGGGNRRTANVVAHGFTNLFILDKKDLNEI
LVGYPERQKLLRKKARRMLRNNNKPKEEKSVJILPPRAGTPKLFNAALAAGKNGPRG
AKGYLAHLRARLKELAALEAAARQQQLLEQAKSSQEAGGEEGSGATDQPAPQEPEP
KDPPKPPGPPEPEPSAGSSPPPASAKPEESTGEAAGPPEPSVRIRVSPGPDPGEQTLSVS
VLEEKKEGAE"
                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 85 Row: 1 Column: 9.
Location/Qualifiers
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                 cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Eye, retina, mouse strain C57Bl\6"
clone_lib="NIH_MGC_94"
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Pred. No. 1.7e-91;
0; Mismatches 508;
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                      Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=2
/product="Cngblb_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="AAH45114.1"
|db_xref="G1:28175675"
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db_xref="MGI:2664102"
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/db_xref="MGI:2664102"
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/db_xref="taxon:10090"
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                                              Score 572.2; DB 4;
Pred. No. 6.7e-91;
0; Mismatches 483;
                                                     Query Match 23.5%;
Best Local Similarity 64.1%;
Matches 862; Conservative
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IPRSVQNRYKTWYEYTVYLPROMYVCKKGEIGERMY IOAGGVOVLGGFDGKSVLYTLKA
GSVFGEISLLAVGGGNRRTANVVAHGFTNLFILDKKDLNBILVHYPESQKLLRKKARR
MENNNKPRSKSVLILDPRAGTPKLFRANALAAAGKOMAKGROGRIALLRARLKELAA
ILEAARKQQULLEQARSSEDAAVGESGSASPEQPPREPPAPERPAPEFLAPER
PAPEAPASSPPASQERPEGDKDAARPEEHPVRIHVTLGPDPSSQILLVEVPEKQEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3083 bp mRNA linear MAM 30-OCT-2001
Bos taurus cyclic nucleotide-gated channel beta subunit 1c
(CNCbeta) mRNA, complete cds.
                            1983 CCAACGTGGTCGCCCATGGCTTCACCAACCTCTTCATACTGGACAAGAAGGACTTGAATG 2042
                                                                                                                                                                                                                                                                                /codon_start=1
/product="cyclic nucleotide-gated channel beta subunit lc"
                                                                                                                      AAATTCTAGTGCATTATCCAGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGCTTT 1936
                                                                                                                                                                                                                                             1937 TAAAGCAGAAGGCTAAGACCGCAGAAAGCAACCCCTCCAAGAAAAGATCTTGCCCTCCTCT 1996
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I (bases 1 to 3083)
I (bases 1 to 3083)
Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and Weyand,I.
                                                                                                                                                                                                                                                                                                                                                                                                2148 TGCCCCCGCGTGCGGGGCACCCCGGAAGCTCTTCAATGCTGCCCCTGGCTGCTGCAGGAAA 2205
                                                                                                                                                                                                                                                                                                                                                              TCCCACCGAAAGAAGACACCCCAAACTGTTTAAAACTCTCCTAGGAGGCACAGGAAA 2054
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      CCAATGTGGTGGCCCACGGGTTTGCCAATCTTTAACTCTAGACAAAAAGACCCTCCAAG
                                                                                                                                                                               2043 AAATITIAGIGCATIACCCGGAATCICAGAAGTIACTICGGAAGAAGAAGCC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclic nucleotide-gated channels on the flagellum control Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-JJN-1998) IBI, FZ-Juelich, Leo-Brandt-Strasse, Juelich, NRW 52425, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 3083)
Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B.
Weyand,I.
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/db_xref="GI:3309622"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bos taurus"
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/db_xref="taxon:9913"
1. .3083
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KTLITIGGLEDPRTLEEIVPGGLNYFTGVPAFSVNIGQMEDVVGAATAGOTYYRSCMD
STYKYMMFYKI PRSVQNRVKTWYEYTHWSCMLDESLMVQLPDKMRLDLAIDVNYSI
VSKVALPGGCDRQMTRUTMYSTYLPNGCMLDESELMVQLPDKMRLDLAIDVNYSI
VSKVALPGGCDRQMTRENLKRLRSVYLPNDYVCKKGEIGREMYIIQAGQVQVLGGPD
GKSVLVTLKAGSVFGEISLLAVGGGNRRTANVVAHGFTNLFILDKKDLNEILVHYPES
OKLLEKKARRMLRNNNKPKEKSVILLPPRAGTPKLFNAALAAAGKWGAKGGRGGLAL
LRARLKELAALEAAARQQQLLEQAKSSEDAAVGEGSASPEOPPRPEPPAPEP
TAPPEPLAPBARAPSSFPPASGSPPAGGERPRGGNKDARPEPPAPEPPPF
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LVEVVPEKQEEKEKKEEETEEKEEGEEARKEKEEE"
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                                                                                                                                                                                                                                                                                                                                          Score 572.2; DB 4; Length 3090; Pred. No. 6.6e-91;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 483;
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DRATSTASQNSAIINDRLQELVKLFKERTEKVKEKLIDPDVTSDEESPKPSPAKKAPE
SPEVKPAEAGQVEEEHY COMLCCKFKRPWKKYOFDQSIDPLTNLMTILWLFEVVLA
WNWNCWLIPVRWAFPYQTPDNIHLWLLMDYLCDLIYLLDITVEQMRLQFVRGSDITTD
KKEMRNNYVKSQRFKWDMLCLLPLDLLYLKFGVNPLLRLPRCLKYWAFFEFNNRLESI
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Bos taurus cyclic nucleotide-gated channel beta subunit 1d
(CNCbeta) mRNA, complete cds.
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OSEVGGAQAGGEVGGAQALSEESETQDQSEVGGAQDQSEVGGAQAQGEVGGAQEQDGV
GGAQDQSTSHQELQEBALADSSGVPATEEHPELQVEDADADSRPLIAEENPPSPVQLP
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protein_id="AAC26128.1"
db_xref="GI:3309624"
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1 (bases 1 to 3090)
Wiesner, B., Weiner, J., Middendorff, R., Hagen, V., Kaupp, U.B. and
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Submitted (24-JUN-1998) IBI, FZ-Juelich, Leo-Brandt-Strasse,
Juelich, NRW 52425, Germany
Location/Qualifiers
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/clone lib="cDNA in plasmid vector pCDNAII (Invitrogen)"
/dev_stage="adult"
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Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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Molecular cloning and expression of the Modulatory subunit of
cyclic nucleotide-gated cation channel
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Submitted (08-JAN-1996) M. Biel, Inst. f. Pharmakologie und
Submitted (08-JAN-1996) M. Biel, Inst. f. Pharmakologie und
Toxikologie, Technische Universitaet Muenchen, 80802 Muenchen,
Biedersteiner Strasse 29, PRG
Location/Qualifiers
                                                           TCCAGTTAGCCCTCGCCATTGATGTGAACTTCAGCATCATCAGCAAAGTCGACTTGTTCA
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/mol_type="mRNA"
/db_xref="taxon:9913"
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/gene="CNG4c"
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GTOQSEVGGAQAQQEEVGBAQALSEESBETODOSEVGGAQDQSEVGGAQAQGEVGGAQQ
GTVGQSQAQQQSTSQELQEBALADDSSGVPTEHPELQVEDADADSRPLIAENPPSP
QDGVGAQQQQSTSQGETQEBALADDSSGVPTEHPELQVEDADADSRPLIAENPPSP
QQLPLSPAKSDTLAVPGSATGSLKRKLPSQDEBAEELKMLSPAASPVVAWSDPTSPQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product="cyclic nucleotide-gated channel beta subunit le"
'protein id="AAC26129.1"
'db_xref="G1:3309626"
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                                            473-484 (1998
                                                                                                                                                                                                                                                                                                                                                                           organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/codon_start=1
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             entry into sperm
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Wiesner, B., Weiner, J.,
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Wiesner, B., Weiner, J., Middendorff, R., Hagen, V., Kaupp, U.B. and
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